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US-09-948-391A-24
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US-09-961-400-24
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SEQ ID NO 24
LENGTH: 110
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US-09-961-400-22
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) Publication No. US2030124131A1
) GENERAL INFORMATION
) APPLICANT: RYBAK, SUSANNA M.
) APPLICANT: RYBAK, SUSANNA M.
) APPLICANT: GOLDENBERG, DAVID M.
) APPLICANT: NEWTON, DIANNE L.
) TITLE OF INVENTION: INMUNOCOMJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
) TITLE OF INVENTION: CELLS
) FILE REPREBENCE: 108733/1059
) CURRENT APPLICATION UNMER: US/09/961,400
) CURRENT FILING DATE: 2001-09-25
                                                                             1 MONWATFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                               1 MONWATFOOKHIINTPIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINLNV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
    0; Gaps
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    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09948391A

Sequence 22, Application US/09948391A

Sequence 22, Application US/09948391A

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: The Wewton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: The United States of America

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

TITLE OF INVENTION NUMBER: US/09/948,391A

CURRENT APPLICATION NUMBER: US/09/948,391A

CURRENT FILING DATE: 1998-03-27

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR PRIOR DATE: 1998-03-26

PRIOR PRIOR DATE: 1998-03-26

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1988-03-27

PRIOR PILING DATE: 1998-03-27

PRIOR PILING DATE: 1998-03-27
    0;
    2; Mismatches
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PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
    109; Conservative
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KENCHL 14

Sequence 24, Application US/09948391A

Sequence 24, Application US/09948391A

Sequence 24, Application US/09948391A

Sequence 24, Application US/09948391A

GENERAL INFORMATION:

APPLICANT: Newton, Disanne I.

APPLICANT: Newton, Disanne I.

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TILE OF INVERTION: Recombinant Anti-Tumor Rase

TILE OF INVERTION: Recombinant Anti-Tumor Rase

TILE OF INVERTION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR APPLICATION NUMBER: WO SCZ,613

PRIOR FILING DATE: 1999-03-26

PRIOR RILING DATE: 1999-03-26

PRIOR RILING DATE: 1999-03-26

PRIOR RILING DATE: 1099-03-26

PRIOR RILING DATE: 1099-03-26

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 43

SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 3.1e-60;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                            Score 601; DB 10;
Pred. No. 1.2e-60;
                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 117
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Best Local Similarity 98.2%;
Matches 109; Conservative
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Best Local Similarity
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US-09-948-391A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                    Score 602; DB 10;
Pred. No. 8.5e-61;
0; Mismatches 1;
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99.1%; Pred. No. 1.1e-60;
iive 0; Mismatches 1;
; PRIOR FILING DATE: 2000-08-17; PRIOR APPLICATION NUMBER: PCT/US99/06641; PRIOR APPLICATION NUMBER: 09.2-26; PRIOR FILING DATE: 1998-03-26; NUMBER OF SEQ ID NOS: 43; SEQ ID NO 26; SEQ ID NO 26; LENGTH: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09948391A Publication No. US20030027311A1
                                                                                                                                                                                                                                                                                    99.2%;
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                                                                                                                                                                                                                ; ORGANISM: Rana catesbeiana
US-09-961-400-26
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.15
Matches 110; Conservative
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Matches 110; Conservative
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                                                                                                                                                                                                TYPE: PRT
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RESULT 7 US-09-948-391A-21

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Sequence 1. Application US/09961400
| Publication No. US20030124131A1
| GENERAL INPORMATION:
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: ROWTON INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT: TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT: TITLE OF INVENTION: UNMERRE. US/09/961,400
| TITLE OF INVENTION: CELLS
| FILE REPRENCE: 2010-08-25
| FILE REPRENCE: 2010-08-25
| FRIOR APPLICATION NUMBER: 09/622,613
| PRIOR APPLICATION NUMBER: PCT/US99/06641
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| NUMBER OF SEQ ID NOS: 43
| COFTWARE PARENT NEW 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbelana ribonuclease with Met at position 1, OCHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant OTHER INFORMATION: Met(-1) RACOR1 Met22Leu Met57Leu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                  APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
TITES OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311003
CURRENT APPLICATION NUMBER: US/09/948,391A
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%; Score 601; DB 10;
98.2%; Pred. No. 1.1e-60;
iive 2; Mismatches 0;
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Pred. No. 1.1e-60;
  Application US/09948391A
Sequence 21, Application US/099.
Publication No. US20030027311A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.0%;
                                                                                   APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.2
Matches 109; Conservative
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ORGANISM: Rana catesbeiana
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Best Local Similarity
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Length 110;

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RESULT 4
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Query Match
Best Local S
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: OELLS
FILE REFERENCE: 018733/1059
CURRENT PAPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PAPLICATION NUMBER: 60/079,751
PRIOR PAPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE PALENTING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana cocyte ribonuclease (RaCOR1) synth OTHER INFORMATION: gene modified to use E. coli preferred codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

99.2%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 8.4e-61;
Matches 110; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                     APPLICANT: Nymeron, Dianne D. APPLICANT: Newton, Dianne D. APPLICANT: The United States of America APPLICANT: The United States of America APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Recombinant Anti-Tumor RNase FILE REFERENCE: 015280-343110US CURRENT APPLICATION NUMBER: US/09/948,391A CURRENT FILING DATE: 1938-03-27 PRIOR APPLICATION NUMBER: WO PCT/US99/06641 PRIOR FILING DATE: 1999-03-26 PRIOR FILING DATE: 1999-03-26 PRIOR FILING DATE: 2000-08-17 NUMBER: OS SEQ ID NOS: 43 SEQ ID NOS: 40 DEATH APPLICATION NUMBER: WO PCT/US99/06050 PRIOR FILING DATE: 200-08-17 NUMBER: OS SEQ ID NOS: 43 SEQ ID NOS: 43 SEQ ID NOS: 43 SEQ ID NOS: 43 DEATH APPLICATION VUMBER: WO PCT/US99/06050 PRIOR FILING DATE: 2.00
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; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
                                                                                                     Sequence 15, Application US/09948391A
publication No. US20030027311A1
PERERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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ORGANISM: Rana catesbeiana
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
                                                                                                                                                                           1 ONWATFOOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
                                                                                                                          2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
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                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NEWTON, Diame L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
TITLE OF INVENTION: 80/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: W5 60/079,751
PRIOR APPLICATION NUMBER: W5 60/079,751
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
               Score 602; DB 10;
Pred. No. 8.4e-61;
99.2%; Scc. 100.0%; Pred. No. c. ... 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.1
Matches 110; Conservative
                                                                                  Matches 110; Conservative
                                                 Similarity
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OM protein - protein search, using sw model

7, 2004, 21:29:40 ; Search time 35.6155 Seconds (without alignments) 865.070 Million cell updates/sec May Run on:

US-09-961-400-17

Perfect score:

1 MQNWATFQQKHIINTPIICN......ICVKCENQYPVHFAGIGRCP 111 Sequence:

Scoring table:

1140673 seqs, 277566755 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USOT_DUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USOT_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USOT_PUBCOMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Op 0	Sequence 17, Appl Sequence 17, Appl Sequence 15, Appl Sequence 26, Appl		Sequence 22, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 19, Appl Sequence 19, Appl Sequence 19, Appl
SUMMARIES	US-09-961-400-17 US-09-948-391A-15 US-09-961-400-15 US-09-948-391A-26	US-US-961-40U-26 US-09-948-391A-17 US-09-948-391A-21 US-09-961-400-21 US-09-961-400-21	US-09-961-400-22 US-09-988-391A-24 US-09-961-400-24 US-09-961-400-19 US-09-948-391A-19 US-09-948-391A-6
DB	100	2001	100000 1111111
% Query Match Length DB	111 011 011 111 111	111	117 110 110 110 110 110
* Query Match	100. 99. 99.2 99.2	0.66	998.0 988.0 44.098.2 7.72
Score	602 602 602 602	601 601 601 601	601 597 597 596 596 590
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61 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111

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11 11 11 11 11 11 11 11 11 11 11 11 11	1 4 4 4 4 1 4 5 6 4 6

ALIGNMENTS

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Sequence 17, Application US/09961400
| Publication No. US20030124131A1
| GENERAL INPORMATION:
| APPLICANT: STBAK, SUSANNA M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: MARWIN, DIANNE L.
| TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: LOGICE.
| TITLE OF INVENTION: CELLS
| TITLE OF INVENTION NUMBER: 09/622,613
| PRIOR FILING DATE: 2000-08-17
| PRIOR APPLICATION NUMBER: 60/079-751
| PRIOR PRILING DATE: 1998-03-26
| PRIOR FILING DATE: 1998-03-26
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Search completed: May 7
Job time: 12.8756 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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6
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45.7%; Score 277.5; DB 3; Length 254;
Best Local Similarity 49.1%; Pred. No. 2.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/08875811

Patent No. 6045733

GRNERAL INFORMATION:
APPLICANT: Ryback, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Widawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:
                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FATIS, SUBAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/POCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/875,811 FILING DATE: US-FEB-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Prancisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 254 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-875-811-61
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US-08-875-811-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 QDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKALCKGIIASKN
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59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                        64 NVLTTSEFYLSDC---NVTSRPCKXKLKKSTNKFCVTCENQAPVHFVGVGSC 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 277.5; DB 3; Length 129; 49.5%; Pred. No. 9.6e-25;
                                                                                                                                                            Sequence 63, Application US/08875811
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
    APPLICANT: Rybak, Susanna M.
    APPLICANT: Newton, Dianne L.
    APPLICANT: Nodawer, Alexander
    TITLE OF INVENTION: Recombinant Ribonuclease Proteins
    NUMBER OF EXQUENCES: 64
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UVERMINGS ISIDEM: PULDOS/RS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 1556-0200
TELERENONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: RYDAK, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 129 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 55; Conserva
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ZIP: 94111-3834
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US-08-875-811-59
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1 MONWATEQOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NM 58
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Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Rybak, Susanna M.
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION TA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US FO/011,800
FILING DATE: 21-FEB-1997
APPLICATION NUMBER: US FO/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.7%; Score 277.5; DB 3; Best Local Similarity 49.1%; Pred. No. 2.2e-24; Matches 55; Conservative 15; Mismatches 33;
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                                                                                                                        SSEE: Townsend and Townsend and Crew LLP

: Two Embarcadero Center, Eighth Floor

San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE-DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 251 amino acids amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                 California
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94111-3834
                                                                                                                                                                                                                                                        ZIP: 94111-3834
                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-875-811-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-875-811-59
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                                                                                                                                                                      STREET:
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2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
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                                                                                                                                                                                                                                                                                                                                                                                                           60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                     Length 104;
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49.1%; Pred. No. 8.1e-25;
tive 15; Mismatches 33; Indels 9
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wodawer, Alexander
ITTLE OF INVENTION: Recombinant Ribonuclease Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAZIS. SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
MATCHER COMMUNICATION INFORMATION:
MEDISCOMMUNICATION INFORMATION
                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                      Query Match
Best Local Similarity 49.5%; Pred, No. 7.4e-25; Matches 55; Conservative 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 32, Application US/08875811 Patent No. 6045793
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TELEPRAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 32
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 amino acids
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Best Local Similarity 49.1<sup>§</sup>
Matches 55; Conservative
                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-095-429-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-875-811-32
STRANDEDNESS:
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US-08-875-811-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09095429
Patent No. 6649393
GENERAL INFORMATION:
APPLICANT: Voule, Richard
APPLICANT: Vasandani, Veena
APPLICANT: Wasandani, Veena
APPLICANT: Boix, Esten
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Allows Production by Recombinant Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 45.7%; Score 277.5; DB 4; Length 1 Similarity 49.5%; Pred. No. 7.4e-25; 55; Conservative 15; Mismatches 32; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,429
                                                                                                                  REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15280-267
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38 589
REFERENCE/DOCKET NUMBER: 15280
TELEPOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acids
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APPLICATION NUMBER: 08/626,288
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-626-288-1
                                                                                                                                                                                                                                                                                                                             TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 55; Conservi
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CLASSIFICATION:
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Gaps

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GENERAL INCORNATION:
APPLICANT: Saxena, Shailendra K
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
TITLE REFERENCE: 50:13 US.01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 QNWAJFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
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                                                                                          60 VLSTTREQLNICTRISITERECPYSSRTETNYLCVKCENQYPVHFAGIGRC 110
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                                                                                                                                                          60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Youle, Richard
APPLICANT: Wo and anni, Veena
APPLICANT: W. You Neng
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Matant Form of Cytotoxic Protein Which
TITLE OF INVENTION: A Matant Production by Recombinant Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.7%; Score 277.5; DB 4; Length 104; 49.5%; Pred. No. 7.4e-25; Indels 9; tive 15; Mismatches 32; Indels 9;
49.5%; Pred. No. 7.4e-25;
Live 15; Mismatches 32; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/08/626,288

PTI-ING DATE: No. 6649392 yet assigned
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
                      15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08626288
Patent No. 6649392
                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09687748 Patent No. 6423515
                        Conservative
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rana pipiens
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Best Local Similarity
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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STATE: Ca
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: NUCLEIC ACIDS
TITLE OF INVENTION: MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 104
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46.0%; Score 279.5; DB 3; Length 358;
Best Local Similarity 49.1%; Pred. No. 2e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9
  APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPRAX: (415) 576-0300
INFORMATION FOR SEC ID NO: 51:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 277.5;
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-394-268-1
; Sequence 1, Application US/09394268
Patent No. 6175003
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.78;
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amino acid
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; ORGANISM: Rana pipiens
US-09-394-268-1
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셤 8 Query Match

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1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
                                   59 NVLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Nodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
TITLE OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: Two mosend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FRB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.0%; Score 279.5; DB 3;
49.1%; Pred. No. 1.9e-24;
iive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 015280-244100US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                   Sequence 41, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION: APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rybak, Susanna M.
Newton, Dianne L.
Boque, Lluis
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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amino acid
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Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                     57
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                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                               DB 1; Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Dianne L.
APPLICANT: Rowcon, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Widdawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
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APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                             46.9%; Score 284.5; DB 1
49.5%; Pred. No. 1.1e-25;
Live 16; Mismatches 31
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CLASSIFICATION NOWER: US/08/875,811
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NOWER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 41,739
TELEPONGUNICATION INFORMATION:
TELEPONGUNICATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6045793
GENERAL INFORMATION:
        Oocyte
                                                                                     Query Match
Best Local Similarity 49.5%
The Solution of the So
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Best Local Similarity 49.1%
Matches 55; Conservative
DEVELOPMENTAL STAGE:
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STATE: California
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US-08-467-955-2
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ORGANISM: Rana pipiens
  ; OTHER INFORMATION:
; OTHER INFORMATION:
US-08-875-811-8
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                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                   Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08875811
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
    APPLICANT: Rybak, Susanna M.
    APPLICANT: Newton, Dianne L.
    APPLICANT: Modawer, Alexander
    TITLE OF INVENTION: Recombinant Ribonuclease Proteins
    NUMBER OF SEQUENCES: 64
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                Indels
                                                                                                                          LOCATION: 1..111
OTHER INFORMATION: /note= "Frog Lectin from Rana
OTHER INFORMATION: catesbeiana"
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                                                                                                                                                                                                                                 Query Match
97.0%; Score 588.5; DB 2;
Best Local Similarity 98.2%; Pred. No. 6.6e-61;
Matches 109; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
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PRIOR APPLICATION UNMBER: WO PCT/US97/02588
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Paine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 111 amino acids
amino acid
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LENGTH: 111 amino acid
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MOLECULE TYPE: protein
                                                 MOLECULE TYPE: protein
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                                                                                                       NAME/KEY: Protein
STRANDEDNESS:
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US-08-875-811-8
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2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
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                                                                                                                                                                                    Score 588.5; DB 3; Length 111; Pred. No. 6.6e-61; 1; Mismatches 0; Indels 1
/note= "Frog Lectin from Rana
catesbeiana"
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/178,118
FILING DATE: 06-APR-1988
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FBB-1992
PRIOR APPLICATION DATA:
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FILING DATE: 01-ABS-1992
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APLICATION NUMBER: US 07/814,332
APLICATION NUMBER: US 07/814,332
APLICATION NUMBER: US 07/814,332
APLICATION UNMBER: US 07/814,332
APLICATION UNMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
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TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERESTICS:
LENGTH: 104 amino acids
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REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
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Best Local Similarity 98.2%;
Matches 109; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REGISTRATION NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
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Sequence 1, Appli
Sequence 2, Appli
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Sequence 8, Appli
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Sequence 1, A
Sequence 1, A
Sequence 32, A
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Sequence 41,
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Sequence 13,
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-875-811-8
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Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
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Sequence 1, Appli Sequence 26, Appl Sequence 28, Appl Sequence 24, Appl Sequence 2, Appli Sequence 2, Appli Sequence 45, Appl Sequence 45, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 24, Appli Sequence 47, Appli Sequence 47, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	Reagents	
4 4 US-09-986-119-1 15 3 US-08-875-811-26 16 3 US-08-875-811-26 17 3 US-08-875-811-24 14 4 US-08-626-288-2 14 4 US-08-626-288-2 14 4 US-09-055-429-2 15 3 US-08-875-811-25 17 3 US-08-875-811-22 18 3 US-08-875-811-22 19 3 US-08-875-811-22 10 3 US-08-875-811-22 10 3 US-09-223-118-2 10 3 US-09-223-118-2 10 3 US-09-223-118-2 10 3 US-09-223-118-2 10 3 US-09-223-118-2 11 3 US-09-223-118-2 12 3 US-09-223-118-2 13 US-09-223-118-2 14 3 US-09-223-118-2 15 US-09-223-118-2 16 US-09-223-118-2 17 US-09-223-118-2 18 US-09-223-118-2 18 US-09-223-118-2	ALIGNMENTS anna M. ard J. anne L. beter J. lective RNase Cytotoxic lective RNase RNase Cytotoxic lective RNase	US 07/510,696
29 272.5 44.9 104 30 272.5 44.9 105 31 272.5 44.9 105 32 272.5 44.9 107 33 269.5 44.4 104 34 269.5 44.4 104 35 268.5 44.4 104 36 268.5 44.4 104 37 250.5 44.2 365 38 250.5 41.3 107 250.5 41.3 107 236.5 38.3 360 40 232.5 38.3 360 41 226 37.4 114 42 225 37.1 114 43 206 33.9 83	1 EAAL INFORMATION: ERAL INFORMATION: ERAL INFORMATION: ERAL INFORMATION: EPLICANT: Youle, RI PPLICANT: Youle, RI PPLICANT: Newton, D FRICANT: Newton, D FRICANT: Newton, D FRICANT: Newton, D FRICANT: Newton, D FREEPONDENCE ADDRES GUTY: San Francisc GUNTER: USA ADDRESSE: Two Embarc GUNTER: USA GUNTER: BALLI-3B34 MEDIUM TYPE: FLORE MEDIUM TYPE: FLORE MEDIUM TYPE: PLORE MEDIUM TYPE: PLORE GOPFRATING SYSTEM: FILING DATE: 22-SEI FILING DATE: 22-SEI FILING DATE: 22-SEI FILING DATE: G16-FEBILING DATE: FILING DATE: 22-SEI FILING APPLICATION NUMBER: FILING DATE: 22-SEI FILING DATE: 22-SEI FILING DATE: 22-SEI FILING DATE: 22-OCC	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0
	RESULT Seed CO	

i: 111 amino acids amino acid

Rana pipiens.

97WO-US002588 96US-0011800P.

19-FEB-1997; 21-FEB-1996;

28-AUG-1997.

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The present sequence is a Rana pipiens Clone 5alb ribonuclease (RaPLRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncoase (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocloxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New recombinant ribonucleases, used for killing target cells, e.g. for
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                                                                                                                                                                                                                                                                                                                              /label= Rana_pipiens_Clone_5alb_ribonuclease
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/label= Signal_peptide
/note= "putative"
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                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0079751P
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es 55; Conservative
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N-PSDB; AAZ08136.
   autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1998;
                                                                        Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                               WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-0CT~1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                            Protein
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NAME OF THE PROPERTY OF THE PR
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RNase A, ribonuclease, cytotoxic, onconase, nonc, immunofusion, tumour cell growth, frog.

R. pipiens recombinant RNase protein [Met-(-1)]rOnc.

(first entry)

20-APR-1998

AAW35123;

AAW35123 standard; protein; 105 AA.

RESULT 15

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AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are modifications of the RNase Onconase (RTM) (nOnc). Such novel ribonuclease molecules are highly cytotoxic and can be used alone or to form chemical conjugates or to target recombinant immunofusions. They are used particularly for decreasing tumour cell growth. They can also be used for cell separation in vitro by selectively killing unwanted types of cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. in bone marrow prior to transplantation into a patient undergoing marrow ablation by radiation, or for killing leukaemia cells or T-cells that would cause graft versus host disease. The toxins can also be used to selectively kill unwanted cells in culture. The new ribonucleases have increased cytotoxic activity compared to none and also lower
                                                                                                                                                                                                                                                                                                  Ribonuclease molecules based on native Onconase - used for killing cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 279.5; DB 2;
49.1%; Pred. No. 5e-24;
Micmarches 32;
                                                                                                                                                                                                           Wlodawer A;
                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 65-66, 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, 2004, 21:38:28
                                                                                                                                                                                                             Boque L,
                                                                                                                                                                                                                                                                                                                       particularly tumour cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.19
Matches 55, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenicity in humans
                                                                                                                                                                                                             Rybak SM, Newton DL,
                                                                                                                                                                                                                                               1997-435168/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: May 7.16 : 47.3489 secs
                                                                                                                                                                                                                                                               N-PSDB; AAT94959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 105 AA;
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LL2 antibody;

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The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein. Carboxy terminal end of RaPHR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Met(-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
                                                                                                                Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody ligand binding moiety; CD22; cancerous B cell; Kaposi; Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.4%; Score 281.5; DB 2; Length 104;
49.5%; Pred. No. 2.9e-24;
live 15; Mismatches 32; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Met(-1) RaPLR1 Gln1Ser amino acid sequence.
                                                                                 Rana pipiens liver ribonuclease (RaPLR1)
                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 55; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY28871 standard; protein; 105
                                                                                                                                                                                                                                                                                                               99WO-US006641.
                                                                                                                                                                                                                                                                                                                                              98US-0079751P.
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                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                     kana pipiens liver
ligand binding ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ08124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 104 AA;
                                                                                                                                                                                                         Rana pipiens
                                                                                                                                                                                                                                                                                                             26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                              27-MAR-1998;
                                                                                                                                                                                                                                          WO9950398-A2
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                                                 25-JAN-2000
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              AAY28865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rana pipiens ribonuclease Clone Salb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 NVLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENOYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 105;
                                                                                                                                        'note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                           /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.4%; Score 281.5; DB 2;
49.1%; Pred. No. 3e-24;
tive 15; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rana pipiens Clone 5alb ribonuclease.
                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY28879 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 34; Page 61; 71pp; English.
                                                                                                                                                                                                                                                                                   99WO-US006641
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                  autoimmune disease; RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                       Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ08129
                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105 AA;
                                                                                                                                                         Misc-difference
                                                     Rana pipiens.
                                                                                                                                                                                                                                                                                   26-MAR-1999;
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                                                                                                                                                                                                                                                  07-0CT-1999
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                                                                      Synthetic
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AAY28879
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Gaps

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'note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                  Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1; CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. for
                                                                                                                                                                                                          'note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                     /note= "Wild type Met replaced with Leu"
                                                               Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                    Location/Qualifiers
standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 59; 71pp; English.
                                                                                                                                                                                                                                                                                                                      99WO-US006641
                                                                                                                                                                                                                                                                                                                                          98US-0079751P
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
N-PSDB; AAZ08127.
                                                                                                                                                                                                                                          Misc-difference 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 105 AA;
                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                     pipiens.
                                                                                                                                                                                                                                                                                                                                           27-MAR-1998;
                                                                                                                                                                                                                                                                           WO9950398-A2
                                          25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                      Rybak SM,
                                                                                                                                                               Synthetic.
AAY28869
                    AAY28869
                                                                                                                                                      Rana
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The present sequence is a recombinant Rana pipiens ribonuclease protein (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective
                                                                                                                                                                                           against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methicnine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MQDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MONWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
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د
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                                                                                                                                                                                                                                                                                                                                                                                           used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.7%; Score 283.5; DB 2;
49.1%; Pred. No. 1.7e-24;
tive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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4

28 95

AAY28865 standard; protein; 104 AA.

AAY28865 ID AAY2

RESULT 11

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Concorded most of the N-terminal or the C-terminal amino acids of mature oncoded most of the N-terminal or the C-terminal amino acids of mature oncomes. The two PCR products generated encoded either the N-terminal 54 amino acids, and were ligated in frame at an Nrul site. The cDNA was then subcloned into a vector e.g., pBluescript, where the ATG initiation codon was ligated to the cDNA. After expression in E. coli, the recombinant the now N-terminal glutamate residue cyclised to form an N-terminal plutamate residue cyclised to form an N-terminal plutamate residue forms part of the phosphate binding pocket of Onconaseand is essential for both ribonuclease and artitumour activity. Onconase is a 12 kD ribonuclease which causes cell death as a result of potent inhibition of protein synthesis by a menanian involving inactivation of cellular RNA. It is not inhibited by mammalian placental ribonuclease inhibitor, which may explain its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agents such as tamoxifen. When used as an anti-tumour agent, Onconase can be conjugated to a marker which targets it to a specific cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour activity against a variety of solid tumours e.g. colon or pancreatic cancers, and can be used alone or in combination with other anti-cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MQNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents recombinant frog Onconase. Onconase has ribonuclease and anti-tumour activity. The cDNA was produced via PCR (using primers AAZ19768-Z19769) of two synthetic DNAs whose sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                     Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         new recombinant Onconase used to treat, e.g. colon cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 282.5; DB 2
50.0%; Pred. No. 2.3e-24;
iive 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                              s;
                   AAY39400 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Leung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                                                                                   99WO-US004252.
                                                                                                                                                                                                                                                                                                                                                       98US-0077557P.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Hansen H,
                                                                                                                                Recombinant frog Onconase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          (IMMU-) IMMUNOMEDICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-551416/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAZ19767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Goldenberg DM,
                                                                                                                                                                                                                                          WO9946389-A1
                                                                                                                                                                                                                                                                                                                   11-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                     11-MAR-1998;
                                                                                                                                                                                                         Rana pipiens
                                                                                            01-DEC-1999
                                                                                                                                                                                                                                                                              16-SEP-1999.
                                                         AAY39400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
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Gaps

6

Indels

32; DB 2;

Length 105;

Query Match

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1 MONWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58
                                                                                                                                           1 MÓDWLTFÖKKHLTNÍRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                   59 NVLSTIRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                         57 NVLTTSEFYLSDC---NVTSRPCKYKLKKSINIFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                     47.2%; Score 286.5; DB 350.0%; Pred. No. 7.9e-25; ive 15; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antitumour protein from Rana pipiens oocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour; chemotherapy; radiotherapy; frog
                                                                                                                                                                                                                                                                                                                             AAW06544 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00467955.
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                   Query Match
Best Local Similarity 50.04
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ALFA-) ALFACELL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-043063/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pipiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9639428-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ardelt WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rana
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                                                                                                                                                                                                                                                                                                        AAW06544
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                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi,'s sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of inbonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                        Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; coalentuly bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                              2 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
(Rana catesbeiana) lectin used to describe the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                             61 LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                      61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                        1;
                                                                                Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Met not found in wild type RaPLR1"
                                                                                                                      Indels
                                                                                Score 588.5; DB 2;
Pred. No. 2.2e-59;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      AAY28867 standard; protein; 105 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 34; Page 57; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0079751P
                                                                                97.0%;
98.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant Met(-1) RaPLR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                    Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoimmune disease.
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAZ08126.
                                        Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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AAY28867;

AAY28867 RESULT

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4,
The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW1824, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW06543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 VLSTTRFQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                              46.9%; Score 284.5; DB 2;
49.5%; Pred. No. 1.3e-24;
tive 16; Mismatches 31;
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AAY28869
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Sequence 105 AA;

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The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human choritonic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                            3 NWAIFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62
                                                                                                                Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; RacOR1 Met221cu, LL2 antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma, human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                              Gaps
                                                            ;
0
                                                                                                                                                          TTRFOLNTCTRISITPRPCPYSSRIBINYICVKCENQYPVHFAGIGRCP 111
                            Length 110;
                                                                                                                                                                            TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                    RaCOR1 Met22Leu Met57Leu amino acid sequence.
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Met replaced with Leu"
                            Score 597; DB 2; I
Pred. No. 2.3e-60;
                                                              ;
0
                  98.4%; Scc...
100.0%; Pred. No....
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; bullfrog; RNase; autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Page 64; 71pp; English.
                                                                                                                                                                                                                                                                       AAY28874 standard; protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US006641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0079751P
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-610847/52.
N-PSDB; AAZ08132.
                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
Sequence 110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                     25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                     Recombinant
                                                            Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                       AAY28874;
                            Query Match
Best Local &
                                                                                                                                                            63
                                                                                                                                                                                                                                                     RESULT
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autoimmune diseases

Sequence 110 AA;

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This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells cytotoxic agent. The products can be used for treating tummors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus contents or infected cells (e.g. cells infected by viruses (sepecially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in vitro by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
                                        ö
                                                                                 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
                                                                                                         1 QNWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLAVUL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytotoxic; RNase, ribonuclease, pancreatic; antibody, light chain; heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; mmune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ď
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinantly fused pancreatic RNase-targeting proteins useful for treating tumors, infections, immune or autoimmune disorders and as
                                                                                                                                                                   62 STTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                      STTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                                          ;
0
Length 110;
                                        0; Indels
  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicholls PJ, Youle RJ;
Score 596; DB 2;
Pred. No. 3e-60;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 19; 47pp; English.
                                                                                                                                                                                                                                                                                                              AAY33321 standard; protein; 111
                                                                                                                                                                                                                                                                                                                                                                                                                                       lectin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90US-00510696.
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    98.2%;
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rybak SM, Newton DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-560488/47.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rana catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-1999
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22-OCT-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-1999
                                          108;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Frog
                                             Matches
                                                                                                                                                                                                                                                                                           AAY3332
                                                                                                                                                                                                                                                                        RESULT
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proteins. They can be used for treatment of cancer and autoimmune

diseases

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                                                                                                                                                                                                                                                          Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LLZ antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a recombinant Rana catesbeiana occyte ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6 tag, Met23Leu and MetSBLeu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion
                                                    9
                                                                  'note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                 1 MONWATFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant ribonucleases, used for killing target cells, e.g. tring cancers, viral infections or autoimmune diseases.
                                                                                            LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                              .,
                                                                                                         LSTTRFQLNTCTRTSITPRFCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                    Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
       Length 111;
                                                                                                                                                                                                                                                                                                                                                                                'note= "Met not found in wild type RaCOR1"
                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Met replaced with Leu"
      Score 602; DB 2;
Pred. No. 6.2e-61;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                      AAY28876 standard; protein; 111 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 66; 71pp; English.
      99.2%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US006641
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                                                                                                                                                                                                               (first entry)
                           110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-610847/52.
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 1
                                                                                                                                                                                                                                                                                                                            catesbeiana.
                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                               25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                            61
                                                                                                                                                                                            AAY28876;
      Query Match
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                  Local
                          Matches
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                                                                                                                                                                       60
                                                                                                                                                                                                                  1 MONWATFQOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; bullfrog; Raposl's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant Rana catesbelana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                 1 MONWATFOOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                           LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
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                                                         Length 111;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild type Gln replaced with Ser"
                       Score 601; DB 2; Len
Pred. No. 8.1e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY28877 standard; protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 22; Page 67; 71pp; English.
                                                                                                          2;
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                                                      99.0%;
98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newton DL;
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                                                                                Similarity
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Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ08134
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                                                                                                          109;
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                                                   Query Match
Best Local S
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                                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
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Sequence 110 AA;

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Recombinant ribonucleases can be expressed in bacteria without an
                   N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moleties to form cytotoxic fusion proteins. They can be used for treatment of cancer and
                                                                                                                                  autoimmune diseases
5555555
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Sequence 111 AA;

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0;
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                                                               MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                             1 MONWATFOOKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV
                                 Gaps
                                                                                                                               61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                 ;
                                                                                                                                              LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
 Length 111;
                                 Indels
 Score 607; DB 2;
Pred. No. 1.7e-61;
                                 Mismatches
                                 .;
0
   100.0%;
100.0%;
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Query Match
Best Local Similarity
Matches 111; Conserv
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AAY28872 RESULT

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AAY28872 standard; protein; 110 AAY28872;

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Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence. (first entry) 25-JAN-2000

Rana catesbeiana oocyte ribonuclease, RaCORI; covalently bound; CD22; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease; RNase.

Rana catesbeiana Synthetic

V09950398-A2

07-OCT-1999

99WO-US006641. 26-MAR-1999;

98US-0079751P 27-MAR-1998; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Rybak SM, Newton DL;

WPI; 1999-610847/52. N-PSDB; AAZ08130.

New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.

for

Claim 22; Page 62; 71pp; English.

The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCORI) protein encoded by a cDNA modified for expression in E. coli. Carboxy terminal end of RaCORI has a covalently bound ligand binding moiety, which can be a LD2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Raposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form approximants disconcer the used for treatment of cancer and autoimmune diseases

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                                                                                                                                                                                                                                                                         Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease GlnlSer; RaCOR1; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; staposi's sarcoma, buman chorionic gonadocrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; CD22; RNase; autoimmune disease.
                                              61
                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                1 ONWAIFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                              2 QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                        Gaps
                                                                                              111
                                                                                                             61 STTREQLNTCTRTSITPRECEYSSRIETNYICVKCENQYEVHFAGIGRCP 110
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                                                                                              62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
 Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Met not found in wild type RaCOR1"
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                                                                      Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
99.2%; Score 602; DB 2; 100.0%; Pred. No. 6.1e-61; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                  AAY28878 standard; protein; 111
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                                                                                                                                                                                                                                (first entry)
                          Matches 110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-610847/52.
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Rana catesbeiana
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                                                                                                                                                                                                                                25-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                          AAY28878;
                                                                                                                                                           RESULT 3
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Sequence 111 AA;

autoimmune diseases

The present sequence is a recombinant Rana catesbelana ribonuclease (RaCORI) protein with Met at position 1 and Gln2Ser. Carboxy terminal end of recombinant RaCORI has a covalently bound ligand binding modery, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and

Claim 22; Page 68; 71pp; English.

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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protein search, using sw model OM protein -

7, 2004, 21:25:55 ; Search time 47.3489 Seconds May Run on:

(without alignments) 662.376 Million cell updates/sec

US-09-961-400-17 607 1 MQNWATFQQXHIINTPIICN......įCVKCENQYPVHFAGIGRCP score: Sequence: Perfect Title:

111

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

1586107

length: 0 length: 2000000000 sed BB BB Minimum I Maximum I

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A Geneseq 29Jan04:* L: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2004s:* .. Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	di.	AAY28873	AAY28872	AAY28878	AAY28876	AAY28877	AAY28874	AAY33321	AAY28867	AAW06544	AAY28869	AAY39400	AAY28865	AAY28871	AAY28879	AAW35123	AAW35125	AAW35130	AAY28866	AAW30301	AAB31666	ABG32650	AAW35118	AAW35134	AAW35135	AAW35133	
	Length DB																355 2									355 2	
% Ouerv	!	100.0	99.2	99.2	0.66	98.4	98.2	97.0	47.2		46.7	46.5	46.4	46.4	46.4	46.0	46.0	46.0	45.9	45.7	45.7	45.7	•	45.7	45.7	45.7	
	Score	607	602	602	0	9	S.	588.5	286.5	284.5	283.5	82.	81.	Ξ.		-	279.5		78.		77.	277.5	77.	77.	77.	277.5	
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Aaw35129 R. pipien	2	Aaw35126 R. pipien	Re	Aar12344 Protein w	Aar47303 ONCONASE	Aaw00736 Protein d	Aaw14065 Onconase	Aaw06543 Antitumou						R.	Aaw35117 R. pipien	U	P.	Aaw35127 R. pipien	Aaw35131 R. pipien
AAW35129	AAW35132	AAW35126	AAY28870	AAR12344	AAR47303	AAW00736	AAW14065	AAW06543	AAW88233	AAY33322	AAB31667	ABG31617	AAW35116	AAW35122	AAW35117	AAW30302	AAW35115	AAW35127	AAW35131
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355	366	379	104	104	104	104	104	104	104	104	104	104	105	106	107	104	105	358	365
45.7	45.7	45.7	45.6	45.2	45.2	45.2	45.2	45.2	45.2	45.2	44.9	44.9	44.9	44.9	44.9	44.7	44.7	44.2	44.2
277.5	277.5	277.5	276.5	274.5	274.5	274.5	274.5	274.5	274.5	274.5	272.5	272.5	272.5	272.5	272.5	271.5	271.5	268.5	268.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1, CD22, covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
                                                                                                                                               Location/Qualifiers
                AAY28873 standard; protein; 111 AA
                                                            Recombinant Met(-1) RaCOR1.
                                             (first entry)
                                                                                                                        Rana catesbeiana.
                                                                                                                                              Key
Misc-difference
                                             25-JAN-2000
                                                                                                                                 Synthetic.
                               AAY28873;
RESULT 1
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/note= "Met not found in wild type RaCOR1"

WO9950398-A2

07-0CT-1999.

99WO-US006641. 26-MAR-1999; 98US-0079751P. 27-MAR-1998;

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WPI; 1999-610847/52.

N-PSDB; AAZ08131

e.g. for New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 63; 71pp; English.

or The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
Beintema J.J.;
"Secretory ribonuclease genes and pseudogenes in true ruminants.";
"Secretory ribonuclease genes and pseudogenes in true ruminants.";
ene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.2%; Score 127.5; DB 1; Length 151; Best Local Similarity 30.6%; Pred. No. 8.7e-07; Matches 37; Conservative 17; Mismatches 44; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | The Property | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 | 1287 |
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16819 MW; 1
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[2]
SEQUENCE OF 31-114 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 NVL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 G 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G 122
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQQKHIINTPI-----ICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC---TGVINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
                                                                                                                                                                                                      -- purification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Gaps
                                                                                                                                                  Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.2%; Score 127.5; DB 1; Length 123; 30.6%; Pred. No. 7e-07; Live 19; Mismatches 43; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 NVLSTTR--FQLNTCTRTSITPR-PCPYSSRTETNYICVKCENQYPVH 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 N-LINKED (GLCNAC. ..).
14522 MW; B703B9839919FD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodom, PD000535, RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNAŠE PANCREATIC; 1
Hydrolase; Nuclease; Endonuclease; Androgenesis;
Protein synthesis inhibitor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  029542; 029533;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giraffa camelopardalis (Giraffe).
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BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyrrolidone carboxylic acid.
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                                                                                                                                        and Serum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
39
113
80
91
          Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giraffidae; Giraffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P10152; 1AGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9894;
                                                           NCBI_TaxID=9913;
                                                                                                                                     TISSUE=Milk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
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ACT_SITE
ACT_SITE
DISULFID
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                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 NITCKNGQPNCYQSNSTWNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :::|:
| AKFRRQHMDSGSSSSSNSNYCNQMMKRR-RMTHGRCKPVNTFVHESLADVKAVCS---QK
MEDLINE-93367815; PubMed-8360916; Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P., Carsana A., Palmieri M., Furia A.; Sequences related to the ox pancreatic ribonuclease coding region in "Sequences related to the ox pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Axis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.

BY SIMILARITY.

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N-LINKED (GICNAC. . .) (BY SIMILARITY).

O-LINKED (BY SIMILARITY).
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Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 127.5; DB 1; Length 141; 30.6%; Pred. No. 8.1e-07;
                                                                                                                          the genomic DNA of mammalian species.";
J. Mol. Bvol. 37:29-35(1993).
-- SUBCELLULAR LOCATION'S Secreted.
-- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73745EFE9079591F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probom, PD000535, American 1.

SMART; SM00092; RNASE PRACEATIC; 1.

PROSTIE; PS00127; RNASE PACEATIC; 1.

Hydrolase; Nuclease; Endonuclease; Glycoprotein.

41

PY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AXIPR
RNBR AXIPR
RNBR AXIPR
P87350;
P87350;
P5-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-PEC-1998 (Rel. 41, Last annotation update)
15-PEC-1998 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 BY
84 BX
84 BX
110 BY
72 BY
62 N-
129 O-
1592 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseBA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRODOM; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S81743; AAB36137.1; -. EMBL; S65126; AAB27931.1; -. HSSP; P00656; 2RNS.
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CAPCA
                                                                                                                                                                                      Beintema J
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P80929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                6 FOOKHI-----INTPLICUTIMDNNIYIVGGOCKRVNTFLISSATTVKALCTGV-INMN 58
                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                               1 QNWATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--
                                                                                                          59 VLSTTRFQLNT-----CTRISITPRP-CPYSSRTETNYICVKCENQ--YPVHF 103
                                                                                                                         67 NGQINCYQSNSTWHIIDCRQIGSSKYENCAXKASQEQKHIIVACEGNPPVPHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 --IGVINMAVLSTTRFQLNTCTRISIT-PRPCPYSSRTETNYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTHYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                              3'-
U-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Probon; PD000535; RNASEA; 1.

R POSITE; PS00127; RNASE PC; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

RW Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

FT HOSTURID 25 80 BY SIMILARITY.

FT DISULPID 39 91 BY SIMILARITY.

FT DISULPID 57 106 BY SIMILARITY.

FT ACT SITE 10 10 BY SIMILARITY.

FT ACT SITE 10 10 BY SIMILARITY.

FT ACT SITE 113 113 BY SIMILARITY.

FT ACT SITE 113 113 BY SIMILARITY.

FT ACT SITE 113 113 BY SIMILARITY.
                                                                                                                                                                                                                                                     Iguana iguana (Common iguana).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                 17;
                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Bloochem. 219:641-646(1994).
--- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphotoligonucleotides ending in C-P or with 2'.3'-cyclic phosphate intermediates.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Pancreas.
--- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                         Score 132.5; DB 1; Length 124; Pred. No. 2e-07;
                                                                                                                                                                                                                                                                          Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana
NCBI_TaxID=8517;
                                                                                                                                                                                                                                                                                                                                          Zhao W., Beintema J.J., Hofsteenge J.;
"The amino acid sequence of iguana (Iguana iguana) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 119;
                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Indels
   0AC28CDE14111845 CRC64;
                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%; Score 131.5; DB 1
30.4%; Pred. No. 2.5e-07;
ive 16; Mismatches 51
                                                                                                                                                                                          119 AA.
                                               Mismatches
                   22.0%; Scor
31.6%; Pred
                                                                                                                                                                                                                                                                                                                      TISSUE=Pancreas;
MEDLINE=94139745; PubMed=8307028;
  13804 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00074, rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001427; RNaseA.
                                            36; Conservative
                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S41111; S41111.
HSSP; P00656; 1LSQ.
  124 AA;
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                   ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                      RNP IGUIG
P80287;
SEQUENCE
                                                                                                                                                                                                                                                                                                              SEQUENCE
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Best Local
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 NITCKNGQPNCYQSNSTWNITDCRQTGSSKYPNCAYKTSQKQKYİTVACEGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ATFQQKHI-----INTPLICNTIMDNNIYLVGGQCKRVNTFIISSATTVKALCTGVINM
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                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Odocolleinae; Capreolus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Secretory ribonuclease genes and pseudogenes in true ruminants.";
Gene 212:259-268(1998).
-!- SUBCELULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
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(BY SIMILARITY).
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Pred. No. 6.8e-07;
                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Edpirolleses, brain (EC 3.1.27.-) (BRB).
Capreolus capreolus (Roe deer).
151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
Anglogenin-2 (EC 3.1.27.-)
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=98278842; Pubmed=9611269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.3%;
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9858;
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ID ANG2_BC
ANG2_BC
DT 01-NOV.
DT 28-FEB-
DE ANG100
GN ANG2.
CC EUKARYC
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Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Blol. Chem. 245:637-653 (1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- TISSUE SPECIFICITY: Pancreas.
-i- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIN; A92071; NRPG.
HSSP: P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoncation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
43; Indels
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N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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Hydrolase, Nuclease, Endonuclease, Glycoprotein.
                                                                                                                                                                                                                  124 AA
 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=70104198; PubMed=4904878;
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=70104197; PubMed=5460946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNASeA; 1.
SMART; SM00022; RNASe PC; 1.
PROSITE; PS00127; RNASE PANCRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00074; rnaseA; 1
  38; Conservative
                                                                                                                                                                                                                   STANDARD;
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CARBOHYD
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   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                            MEDLINE=92093604; PubMed=1754384; Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S., Viola M., Palmieri M., Russo E., Furia A.; "Molecular cloning of the gene encoding the bovine brain ribonuclease and its expression in different regions of the brain."; Nucleic Acids Res. 19:6469-6474(1991).
                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria, Cetartiodactyla; Ruminantia, Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                       Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y., Ohgi K., Irie M., "Primary structure of a ribonuclease from bovine brain."; J. Biochem. 104:939-945(1988).
                                                                                                                                                                                                                                                                                                             [3]
SEQUENCE OF 27-167 FROM N.A.
MEDLINE=96139017; PubMed=8587129;
Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.;
"Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 133.5; DB 1; Length 167; Pred. No. 2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                  T. Mol. Evol. 41:850-858(1995).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
SIGNAL
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681CAAC3CC2FC459 CRC64;
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N-LINKED (GLCNAC. ..).
/FIIG-CAR_000005.
                                                                                                                                                                                                                      SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIBONUCLEASE, BRAIN.
      16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (BC 3.1.27.-) (BRB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O-LINKED.
                                                                                                                                                                                                                                                 MEDLINE=89214015; PubMed=3243767;
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159 O.
155 T
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GlycoSuiteDB; P39873; -.
InterPro; IPR001427; RNSSEA.
Pfam; PPG0074; rnsSeA; 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%;
31.4%;
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167 AA;
                                             Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                      SEQUENCE FROM N.A.
                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                     TISSUE=Brain;
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88 NITCKNGHPNCYQSKSIMSIIDCREIGSSKYPNCAYKISQKQKYIIVACEGNPYVPVHFD 147
                                                                                                                                                               58 NVL------STTREQLNTCTRISITERP-CPYSSRTETNYICVKCE-NQY-PVHFA 104
4 ATFQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGVINM 57
                                                                     32 AKFRRQHMDSGSSSSSNPNYCNQNMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.; "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence."; FEBS Lett. 31:181-185(1973).
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"The primary structure of porcine pancreatic ribonuclease. 3. The disulfide bonds."
J. Biol. Chem. 245:654-661(1970).
J. CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphares and 3'-phosphare) phosphares and 3'-phosphare intermediates.
With 2', 3'-cyclic phosphare intermediates.
J. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
NCBI_TaxID=9823;
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TISSUE=Serum;
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RNBR_BOVIN
ID _RNBR_BOVIN
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RY STAIN=FVB/N; TISSUE=Liver;

RX ALSIN=2438257; PubMed=12477932;

RA ALSCHN=248257; PubMed=12477932;

RA ALSCHNI S.F., Feingold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Botchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pabey J., Helton E., Ketteman M. Madan A., Rodrigues S., Sanchez A.,

RA Blacksley R.W., Toung A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Saklska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 FQQKHII-----NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 LCKNGRINCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                   | F.L.W. | PRINTS; PRUU.>., | PRUM.>., | PRUM.>., | PRODOM; PD000535; RNasea, | ... | PRODOM; PD000535; RNase Pc, 1. | & PROSITE; PS00127; RNASE PACREATIC, 1. | ... | PROSITE; PS00127; RNASE PANCREATIC, 1. | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ... | ..
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01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
                                                                                                                                                                                                                                                                                                                                                                                           Score 135.5; DB 1; Length 124;
Pred. No. 9.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bond M.D., Vallee B.L.; "Isolation and sequencing of mouse angiogenin DNA."; Blochem. Blophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                     39;
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 9.7e-
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91025023; PubMed=2222458;
PIR; A00818; NRWHK.
HSSP; P00656; 1SRN.
InterPro; IPRO1427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                           22.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANGI MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 CKDVNÍFIHGNKSNIKAĽCGANGSPYRENLRMSKSPFOVTÍCKHIGGSPRPPCOYRASAG 122
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                                                                                                                                                                                                                                           Biochim. Biophys. Acta 1162:177-186 (1993).

-I-FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.

-SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRINTS; PR00792; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                        MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
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human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(Rel. 31, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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BY
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EMBL, BCO55355, AAH55355.1; -.
PIR; A35932, A35932.
HSSP, P03950, 1A4Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 FRHVVIACENGLPVHF 138
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39.5%;
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InterPro; IPR001427; RNaseA.
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137
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                                                                                PARTIAL SEOUENCE.
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01-FEB-1995
01-FEB-1995
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SIMILARITY: Belongs to the pancreatic ribonuclease family
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145 AA;
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ACT_SITE
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 CKRVNTFIISSATTVKAIC-----TGVINMNVLSTTRFQLNTCTRISITPR-PCPYSSR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=129; TISSUE=Liver;
MEDLINE=96079109; PubMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes.";
Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                             FUNCTION: Anglogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity). SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                  SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                           25.7%; Score 154.5; DB 1; Length 145; 43.6%; Pred. No. 1e-09; ive 12; Mismatches 23; Indels 9;
developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                            DE9D3BC92F1D682C CRC64;
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41, Last annotation update)
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                    Mol. Cell. Biol. 17:1503-1512(1997)
                                                                                                                                                                                MGD; MGI:1201793; Angl.
MGD; MGI:1201793; Angl.
InterPro; IPRO01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
Probom; PD000535; RNaseA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                           16696 MW;
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115
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64
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                                                                                                                                                                                                                                                                                                                                                                                                          145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Q64438;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 CKRVNTFIISSATTVKAIC---IGVINMNV-LSTTRFQLNTCTRTSITPR-PCPYSSRTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Cetacea, Mysticeti,
Balaenopteridae, Balaenoptera.
NCBI TaxID=9767;
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-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3'-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANGIOGENIN-RELATED PROTEIN.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Balaenoptera acutorostrata (Minke whale) (Lesser rorqual)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 3.6e-09; 10; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00127; RNASE_PANCREATIC; 1.
Signal; Hydrolase; Nuclease; Endonuclease;
Pytrolidone carboxylic acid.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 149.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=76277855; PubMed=962870;
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || : ||| : ||||
|123 FRYIIIGCENGWPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16612 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 INYICVKCENQYPVHF 103
                                                                                                                                                                                                                                                                 EMBL; U22519; AAA91367.1; -.
                                                                                                                                                                                                                                                                                                                          MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00092; RNAse Pc; 1
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1 QNWAIFQQKHIINI-PIICNTIMDNNIYIVGGQCKRVNIFIISSATIVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ODWLTFOKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
-!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
                                                           -!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PDB; 10NC; 31-JAN-94.
InterPro; IPR001427; RNaseA.
Pfam; PP000074; rnaseA; 1.
Probom; PD0000535; RNaseA; 1.
Probom; PR000072; RNase P; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANGE ()?
ANGE, OR ANGE,
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
: (EC 3.1.27.-) (Angiogenin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fu X., Kamps M.P., "E2a-Pbx1 induces aberrant expression of tissue-specific and
                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                          SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.5%; Pred. ....
tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.1%; Score 277.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c;
MEDLINE=97184476; PubMed=9032278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                          Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenin-3 precursor
                                                                                                                                                                                                                                                                                    104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ONWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 60
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens occytes and early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94166079; PubMed=8120892;
Mosimann S.C., Ardelt W., James M.N.G.;
"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
amphibian ribonuclease with anti-tumor activity.";
J. Mol. Biol. 236:1141-1153(1994).
        -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphate intermediates.
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens
oocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG.-1991 (Rel. 19, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
P-30 protein (EC 3.1.27.-) (Onconase).
Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Anura, Neobatrachia, Ranaidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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MEDLINE-93066156, PubMed=1438177;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                          Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                   Length 111;
                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                               27; Indels
                                                                                                                                                                                                                                                                                                                                                   D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               Score 374; DB 1;
Pred. No. 2.1e-33;
                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                               9; Mismatches
                                                                                                      HSSP, P11916, 1BC4.
InterPro; IPR001427; RNaseA.
InterPro; IPR001427; RNaseA.
Pfam; PD00054; RNaseA; 1.
SWART; SM00092; RNase Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                    PROBABLE
                                                                                                                                                                                                                                                                                                                                                  12461 MW;
Biochem. 106:729-735(1989)
                                                                                                                                                                                                                                                                                                                                                                                 62.1%;
65.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins 14:392-400(1992).
                                                                                                                                                                                                                                                                                                                                                                                                               73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                      10
35
104
72
82
                                                                                         PIR; JX0085; JX0085.
                                                                                                                                                                                                                                                                                                                                                   111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             James M.N.G.;
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                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
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residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including
                                                                                                                                                                                                                                                                               Pfam, PP00074; rnaseA; 1.
Prodom; PD000535; RNaseA; 1.
SMART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                              normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133
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                                                                                   SUBCELLULAR LOCATION: Secreted. SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 591.5; DB 1; Length 133; Pred. No. 1.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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14762 MW; A7D62594F7D16F0C CRC64;
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                                                                                                                                                                                                                                                                                                                                            Signal, Pyrrolidone carboxylic acid.
SIGNAL 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.18;
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                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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01-FEB-1994
10-OCT-2003
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P18839;
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ID LECS R1
AC P18839;
DT 01-NOV-
DT 01-FEB-
DT 10-OCT-
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Created)
Last sequence update)
Last annotation update)

(Rel. 16, (Rel. 28, 1)

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                                                                                                                                                                                                         FUNCTION: The S-lectine in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes. SUBUNIT: Moroomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QNWAKFQEKHIPNTSNINCNTIMDKSIYIVGGQCKERNTFIISSATTVKAICSGASTNRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y., Okazaki T., Ohgi K., Irie M.; "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                            Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H., Takayanagi Y., Titani K.,
                                                                                                                                                                    'Amino acid sequence of a lectin from Japanese frog (Rana japonica)
Sialic acid-binding lectin (EC 3.1.27.-).
Rana japonica (Japanese reddish frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordaťa, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBI_TaxID=8400,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 VLSTTRFOLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VLSTTRFQLNTCIRSATAPRPCPYNSRTETNVICVKCENRLPVHFAGIGRC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 455; DB 1;
Pred. No. 4.1e-42;
7; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclesse, liver (BC 3.1.27.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.6%; Score 455;
                                                                                                                                                                                                                                                                                                                                                 INCEPPO; IPRO01477; RNaseA.
Pfam, PF00074; rnaseA; 1.
Prodom, PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
MEDLINE=90130374; PubMed=2613682;
                                                                                                        TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
                                                                                           SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                   Biochem. 108:139-143(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
10
35
104
72
82
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                                                                                                                                                                                                                                                                                                                        PIR; JX0120; JX0120.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                         NCBI_TaxID=8402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPL RANCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
ACT_SITE
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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GenCore version 5.1.6
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OM protein - protein search, using sw model

May Run on:

7, 2004, 21:30:40 ; Search time 5.55659 Seconds (without alignments) 1030.796 Million cell updates/sec

US-09-961-400-15 602 1 QNWATFQOKHIINTPIIGNT.....ICVKGENQYPVHFAGIGRCP 110 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P11916 rana catesh	9 rana	rana		mus m	mus	bala		pog				o.		0		'n		m	Q8wn66 cercopithec		P00676 myocastor c	P00683 mus musculu	Q8wn61 aotus trivi	Q8wn67 pongo pygma	P31346 sus scrofa	P00679 cavia porce	2 saguin	4	0	PO4059 proechimys		Q8wn63 macaca mula
SUMMARIES	DI	RNPO RANCA	LECS RANJA	RNPL_RANCA	RN30 RANPI	ANG3 MOUSE	ANGR_MOUSE	RNP BALAC	ANGI MOUSE	RNBR BOVIN	RNP PIG	RNP_IGUIG	RNBR CAPCA	ANG2_BOVIN		RNBR_AXIPR	ANGI_SAISC	ANGI_MIOTA	RNBR SHEEP	RNP_ANTAM	ANGI_CERAE	RNP_MACRU	RNP_MYOCO	RNP_MOUSE	ANGI_AOTTR	ANGI_PONPY	ANGI_PIG	RNPB_CAVPO	ANGI_SAGOE	RNP_HORSE	RNP_CAMDR		- 1	ANGI_MACMU
	Length DB	1 8	111 1			145 1	145	124	145	167	124	119	151	123	141	151	146	G	m	124	146	122	128	149	146	147	123	128	146	128	124	æ	on .	
•⁄•	Query Match	98.3	75.6	62.1	46.1		24.8	22.5	22.5	22.2	22.0	21.8	21.3	21.2	21.2	21.2	20.8	20.6	20.5	20.3	20.3	20.3	20.0	20.0	19.9	19.9	19.9	19.7	19.6	19.5	19.4		19.2	
	Score	591.5	455	374	277.5	154.5	149.5	135.5	135.5	133.5	132.5	131.5	128.5	127.5	127.5	127.5	125	124	123.5	122.5	122.5	122	120.5	120.5	120	120	119.5	118.5	118	117.5	116.5	16.	115.5	
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P10152 bos taurus	200660 rangirer ca Q8wn64 papio hamad	P03950 homo sapien	Q8wme8 pan troglod	P00664 capreolus c	P00662 giraffa cam	Q9jjh1 mus musculu	P31347 oryctolagus	P24717 cricetulus	O55004 rattus norv	Q9wtt5 acomys cahi
ANGI BOVIN	ANGI PAPHA	ANGI HUMAN	ANGI_PANTR	RNP_CAPCA	RNP_GIRCA	RNS4 MOUSE	ANGI RABIT	RNP_CRILO	RNS4 RAT	RNP_ACOCA
٦,			Н	Н	Н	Н	Н	Н	Н	Н
148	146	147	147	124	124	148	125	130	147	149
18.9	18.9	18.8	18.8	18.7	18.7	18.7	18.6	18.5	18.5	18.5
114	113.5	113	113	112.5	112.5	112.5	112	111.5	111.5	111.5
3.4 4.5	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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pancreatic ribonuclease (BC 3.1.27.5) B - guinea pig (tentative sequence)
NyAlternate names: RNase IB
NyAlternate names: RNase IB
C;Becies: Cavia porcellus (guinea pig)
C;Date: 24-Appr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;Van den Bergy, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a A;Reference number: A91247; MUID:77185023; PMID:862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 evAn.
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Reywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 FOOKHI-----INTPLICUTIMDNNIYIVGGOCKRVNTFIISSATTVKALCTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKRVNTFIISSATTVKAICTG----VINMNVLSTTRFQLNTCTRISITPR-PCPYSSRTE 87
                                  | | | | | | | : | | | | : | | | | : | | | | : | | | | CKEVNTFIHGTRNDIKAICNDKNGEPYNNFRRSKSPFQITTCKHKGGSNRPPCGYRAIAG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----STIRFQLNTCIRISITPRP-CPYSSRIEINYICVKCENQ--YPVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 LCKNGQTNCYQSYSRMRITDCRVTSSSKFPNCSYRMSQAQKSIIVACBGDPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.7%; Score 118.5; DB 1; Length 128; Best Local Similarity 31.6%; Pred. No. 8.5e-05; Matches 37; Conservative 14; Mismatches 43; Indels 23;
                                                                                                                             88 TNYICVKCENQYPVHF 103
                                                                                                                                                                                     99 FRTIAVACENGLPVHF 114
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Search completed: May 7, 2004, 21:54:55 Job time: 10.9813 secs

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mouse angiogenins: discernme:
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A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
A;Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific A;Reference number: S22598; MUID:92107684; PMID:1840677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 FQQKHI-----INTPLICUTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-149 < csAM.
A; Residues: 1-149 < csAM.
A; Cross-references: EMBL: X60103; NID: 953981; PIDN: CAA42697.1; PID: 953982
R; Lenstra, J. A.; Beintema, 36, 399-408, 1979
R; Lenstra, J. A.; Beintema, 98, 399-408, 1979
A; Title: The amino acid sequence of mouse pancreatic ribonuclease.
A; Reference number: A00830; MUID: 80024269; PMID: 556267
A; Reference number: A00830
A; Molecule type: protein
A; Residues: 26-149 < LEN>
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F; 26-149/Product: pancreatic ribonuclease #status experimental < NAT>
F; 26-149/Product: pancreatic ribonuclease #status experimental < NAT>
F; 26-144/Active site: His, Lys, His #status predicted
F; 51-109, 65-120, 83-135, 90-97/Disulfide bonds: #status predicted
F; 62, 87/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                           pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse
NiAlternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30.Nov-1980 #sequence mouse)
C;Accession: A34090; S2258; A00830
B;Schweller, C; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Nol. Biol. Evol. 7, 29-44, 1990
A;Fitle: Evolution of nucleic acids coding for ribonucleases: the mRNA seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 FORQHMDPDGSSINSPTYCNOMMKRR-DMTNGSCKPVNTFVHEPLADVQAVCS---QENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: this sequence was submitted to the Protein Sequence Database, C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig
A;Reference number: S29833; MUID:93192291; PMID:8448182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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Pred. No. 6.5e-05;
6; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20.0%; Score 120.5; DB 1, 30.8%; Pred. No. 6.3e-05; ive 16; Mismatches 42.
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39.5%;
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nes 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: S22598
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                    A;Accession: A34090
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asharesiace identes rauses a processor oxygus ("Species: Myocastor coypus (untria, coypu) ("Species: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000 ("Accession: A00822 Ryvan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J. Ryvan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J. Ryvan den Biophys. Acta 453, 400-409, 1976 A.; Philo: 99896 A.; Accession: Apreference number: A90612; MUD: 77065676; PMID: 99896 A; Accession: Ao0822 A.; Molecule type: protein A; Residues: 1-128 <VAN>C; Superfamily: pancreatic ribonuclease C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas C; Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F; 12,41,119/Active site: His, Lys, His #status predicted F; 26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental F; 34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                      62 NVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAXKTTQAKKHIIVACEGNFYVPVHY 120
AKFERQHIDSNPSSVSSSNYCNQMMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61
                                                                STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 LCKNGQTNCYQSNSNMHITDCRVTSNSDYPNCSYRTSQBEKSIVVACEGNPYVPVHF 120
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                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 FOROHMDTEHSTASSSNYCNLMMKAR-DMTSGRCKPLNTFIHEPKSVVDAVCHQENVTCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 TGVINMNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQY-PVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 NGRINC-YKSNSRLSIINCRQIGASKYPNCQYETSNINKQIIVACEGQYVPVHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A00833
R;Gastra, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of Kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 FQQKHI-----INTPLICUTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 122; DB 1;
Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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30.7%; Pre
tive 16;
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Best Local Similarity
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                                                                          58 NVL----
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Gaps

17;

Indels

42;

Length 124;

28 99

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A,Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A,Reference number: A00813; MUID:80075014; PMID:513141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pancreatic ribonuclease - common iguana

C;Species: Iguana iguana (common iguana)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998

C;Accession: S41111

R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.

Eur. J. Biochem. 219, 641-646, 1994

A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
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C,Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental F;26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                       6 FQQKHI-----INTPILCNTIMDNNIYIVGGQCKRVNTFIISSATTVKALCTGV-INMN
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C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Peb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gaastra, W.; Munniksma, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QNWATFQQKHI-----INTPLICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAIC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                               59 VLSTTRFQLNT-----CTRISITPRP-CPYSSRTEINYICVKCENQ--YPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 NGOTNCYQSNSTWHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF
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                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.8%; Score 131.5; DB 2;
30.4%; Pred. No. 4e-06;
Live 16; Mismatches 51;
                                                                                                                                                                                    22.0%; Score 132.5; DB 1
31.6%; Pred. No. 3.3e-06;
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30.3%; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 30.3%; Pred. No. 3.3e.
Conservative 18; Mismatches
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A;Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
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C; Superfamily: pancreatic ribonuclease
                                                                                                                                         Query Match
Best Local Similarity 31.0.
-hog 36; Conservative
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Best Local Similarity
Matches 35; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        A)Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R;Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A;Title: Primary structure of a ribonuclease from bovine brain.
A;Reference number: JX0056; MUID:89214015; PMID:3243767
                                                                                                                                                                                                                                             ê
                                                                                                                                                                      M.; Palmieri
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A;Residues: 1,'Q',3-124 <UAC>
R;Wierenga, R.K.; Huizinga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A;Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
pancreatic-type ribonuclease (EC 3.1.27.5) BRb precursor, brain - bovine (Species: Bos primigenius taurus (cattle) (chattle) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď
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A;Accession: A91391
A;Wolceule type: protein
A;Residues: 1-124 <WIE>
B;Phelan, J-1; Hirs, C.H.W.
J, Biol. Chem. 245, 654-661, 1970
J, Biol. Chem. 245, 654-661, 1970
J, Ritle: The primary structure of porcine pancreatic ribonuclease. III. The disulfide PA;Reference number: A92072; MUID:70104198; PMID:4904878
A;Contents: annotation; disulfide bonds
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 27-154,'S',156-166 < WAT>
A; Residues: 27-154,'S', 156-166 < WAT>
A; Residues: 27-154,'S', 156-166 < WAT>
A; Experimental source: brain
C; Superfamily: pancreatic ribonuclease
C; Keywords: glycoprotein; hydrolase
F; 38, 67,45/Active site: His, Lys, His #status predicted
F; 38, 67,45/Active site: His, Lys, His #status predicted
F; 88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 155/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 133.5; DB 2
Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Conservative
                                                                                                                                                                                                                                                                                A,Accession: S20066
A,Molecule type: DNA
A,Residues: 1-167 <SAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: JX0056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 G 105
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Gaps

Length 119;

51 59 7;

Gaps

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pancreatic ribonuclease.

experimental

7;

23;

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A.Residues: 1-155 <- 2000>
A.Residues: 1-155 <- 2000>
A.Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C.Genetics:
A.Introns: #status absent
A.Introns: #status absent
C.Function: Apperaintly: pancreatic ribonuclease
C.Superfamily: pancreatic ribonuclease
C.Superfamily: paroreatic ribonuclease
C.Keywords: anglogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F.1-24/Domain: signal sequence #status predicted <- NAT>
F.25-145/Product: anglogenin #status predicted <- NAT>
F.35-Nodified site: anglogenin #status predicted (Gln) (in mature form) #status predicted
F.37, 64, 137/Active site: His, Lys, His #status predicted
F.50-104, 63-115, 81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQQKHII-----NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 FOR DHMDSGNSPGNNPNYCNOMMARR-KWITQGRCKPVNIFVHESLEDVKAVCS---QKNV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anglogenin precursor - mouse anglogenesis factor
NyAlternate names: anglogenesis factor
NyContains: ribonuclease (EC 3.1.27.-)
Cypecies: Mus musculus (house mouse)
Cypecies: Mus musculus (house mouse)
Cypecies: Musculus (house mouse)
AyTitle: Isolation and sequencing of mouse anglogenin DNA.
AyReference number: A35932; MUID:91025023; PMID:2222458
AyAccession: A35932
AyStatus: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 L-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LCKNGRINCYBSNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRISITPR-PCPYSSRTE
     N;Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                     A;Residues: 1-124 <EMM>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancre
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancre
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;76/Binding site: carbohydrate (Asn) (covalent) (partial) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 124;
                                                                           C;Accession: A00818
C;Accession: Melling, G W.; Beintema, J.J.
R;Emmens, M.; Welling, G W.; Beintema, J.J.
Biochem. J. 157, 317–323, 1976
A;Title: The mains acid sequence of pike whale (lesser rorqual)
A;Reference number: A00818; MUID:76277855; PMID:962870
A;Reference rorderin
A;Molecule type: protein
A;Residues: 1-124 < EPMA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                               22.5%; Score 135.5; DB 1
33.3%; Pred. No. 1.7e-06;
iive 16; Mismatches 39
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ilarity 39.5%; Pred. No. 2e-06;
Conservative 12; Mismatches
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RNase 1; RNase
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123 FRHVVIACENGLPVHF
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Best Local Similarity
Matches 30; Conserv
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Best Local S:
Matches 39
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                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (BC 3.1.27.5) - bullfrog
C;Species: Rana catesbelana (bullfrog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C;Accession: 070085
R;Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Usintta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Usinte, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Usinterence number: JX0085, MuID:90130374; PMID:2613682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
ribonuclease. Rana pipiens (northern leopard frog)
c;Species: Rana pipiens (northern leopard frog)
c;Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C;Accession: A39035
R;Ardelt, W: Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A;Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and expresence number: A39035; MUID:91093131; PMID:1985896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QNWATFQQKHIINTFII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ONWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK
        QNWATFQQKHIINTP-IICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMN
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Superfamily: pancreatic ribonuclease
C.Keywords: hydrolase; pyroglutamic acid
C.F.Moddiffed site: pyrrollidone carboxylic acid (Gln) #status experimental
F:10,35,104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 VLSTTREQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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48.6%; Pred. No. 2.1e-20;
iive 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 374; DB 2;
Pred. No. 2.9e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - minke whale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Accession: A39035
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-104 <ARD>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pancreatic ribonuclease (EC 3.1.27.5)
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65.8%;
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Best Local Similarity 65.u.
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A; Residues: 1-111 <NIT>
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Matches 54; Conserv
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Indels

29;

Length 145;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

7, 2004, 21:38:36; Search time 9.98129 Seconds May Run on:

(without alignments)
1060.090 Million cell updates/sec

US-09-961-400-15

602 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Perfect score: Seguence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: Pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 2 8 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

angiogenin precurs pancreatic-type ri pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc anglogenin precurs pancreatic ribonuc anglogenin - rabbi pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc ribonuclease-relat ribonuclease-relat pandreatic ribonud pancreatic ribonuc pancreatic ribonuc ribonuclease-relat pancreatic ribonuc pancreatic ribonuc angiogenin - pig pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pandreatic ribonud _ dom angiogenin [valida ribonuclease Description SUMMARIES A27121 JX0120 JX0085 A39035 A39035 NRWHK A35932 S20066 B43825 S22808 NRBOB П Query Match Length DB Score 588.5 133.5 132.5 131.5 122.5 122.5 120.5 119.5 119.5 1118.5 1116.5 1116.5 1116.5 1116.5 112.5 112.5 112.5 112 111.5 274.5 135.5 135.5 113.5 Result No.

pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc eosinophil-derived pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc pancreatic ribonuc seminal ribonuclea seminal ribonuclea seminal ribonuclea pancreatic ribonuc
NEEKN SO7141 NRBO 161900 NRSH JX0115 NRCB NRCP NRRY NRRY NRRY NRRY NRRY NRRY NRRY NRR
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124 124 124 125 125 125 125 125 125 125 125 125 125
11888888888888888888888888888888888888
1110.5 1110.5 1110.5 1110.5 1110.5 1008.5 1008.5 1006.5 1006.5 1004.5 1004.5
888888888844444 01188459788890118845

ALIGNMENTS

RESULT 1	
A27121	
ribonucl C:Specie	ribonuclease-related sialic acid-binding lectin - bullfrog C.Species: Rana catesbaiana (hullfrom)
C;Date: C;Access	C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993 C:Accession: A27121
R;Titani Biochemia	R,Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag Biochemistry 26, 2189-2194, 1987
A,Title: A,Refere	A,Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana) A,Reference number: A27121; MUID:87299649; PMID:3304421
A; Molecui	A;Accession: A27121 A;Molecule type: protein
A; Residue	A;Residues: 1-111 <tit></tit>
C;Superfa C;Keyword	C;Superfamily: pancreatic ribonuclease C;Keywords: lectin
Query Match	97.88;
Best Lo Matches	Pred. No. 1.4e-51; 1: Mismatches 0. Tudol
	in the state of th
λŏ	1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINNNV 59
ДD	1 ENWATFOQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
δ	60 LSTTRPQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
дС	61 LSTTRFQLNTCIRTSITPRFCPXSSRTBINYICVKCENQYPVHFAGIGRCP 111

JX0120

CiSpecies: Rana japonica (Japanese frog)
CiAccession: JAC-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CiAccession: JAC-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CiAccession: JAC-1990 #sequence of a lectin from Japanese frog (Rana japonica) eggs.
A:Reference number: JAC-1990; MUID:91035319; PMID:2229005
A:Reference number: JAC-2090 MID:91035319; PMID:2229005
CiSpecial type: protein
A:Residues: 1-111 cKAM>
A:Residues: 1-111 cKAM>
CiSuperiamily: pancreatic ribonuclease
CiSuperiamily: pancreatic ribonuclease
CiSuperiamily: pancreatic ribonuclease
CiSuperiamily: pyroglutamic acid
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Gaps 5 Query Match 75.6%; Score 455; DB 1; Length 111; Best Local Similarity 78.4%; Pred. No. 2.6e-38; Matches 87; Conservative 7; Mismatches 15; Indels

2

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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-875-811-41
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                                                                                                                                                                           1 ONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                   59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                         6
                                                                                                     Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.6%; Score 274.5; DB 3; Length 105; 48.6%; Pred. No. 1.7e-24;
LOCATION: 1..104
OTHER INFORMATION: /label= Onc
OTHER INFORMATION: /note= "Onconase from Rana pipiens"
                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.
APLICANT: Newton, Dianne L.
APLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,08/875,811
                                                                                                 45.6%; Score 274.5; DB 2; allarity 48.6%; Pred. No. 1.7e-24; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Enbarcadero Center, Eighth Floor
STREE: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 41,739
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: US/08/875,811
19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                 Query Match
Best Local Similarity
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Matches 54; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-08-875-811-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: C:
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-875-811-39
                                                           US-08-891-848-13
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                                                                                                                                       Matches
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1 QNWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58

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2 EDWLTFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                             59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                           59 VLSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.6%; Score 274.5; DB 3; Length 355; 48.6%; Pred. No. 7.7e-24; tive 16; Mismatches 32; Indels 9
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7, 2004, 21:40:45
                                                                                                                                                                                                                  Sequence 41, Application US/08875811 Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 48.6
Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two Engage CITY: San Francisco CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: May 7
Job time: 13.7596 secs
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N-terminal
FRAGMENT TYPE:
ORIGINAL SOURCE:
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                                                                  ;
US-08-467-955-1
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08467955;
Parent No. 5728805;
GENERAL INFORMATION:
APPLICANT: AACALL Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE Mark H. Jay, P.A.
STREET: P.O. Box E
CITT: Short Hills
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                          59 VLSTIRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                         6
                                                                                                                                              45.6%; Score 274.5; DB 1; Length 104; ilarity 48.6%; Pred. No. 1.7e-24; Conservative 16; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
FRIOR APPLICATION: 435
FRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
FRIOR APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: JAY, MARK H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 2000 US
TELEGOMPHICATION NUMBER: 27507
FREENENCE/DOCKET NUMBER: 2000 US
TELEGOMPHICATION NUMBER: 2000 US
TELEGOMPHICATION NUMBER: 2000 US
TELEGOMPHICATION NUMBER: 2000 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: NO: 5728865 Applicable
INFORMATION FOR SEQ ID NO: 1:
        FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                        Query Match
Best Local Similarity
Matches 54; Conserv
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  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-08-467-955-1
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1 EDWLIFQKKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
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                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                              57 VLITSEFYLSDC---NVISRPCKYKLKKSINKFCVTCENQAPVHEVGVGSC 104
                                                                                               ch 45.6%; Score 274.5; DB 1; Length 104; I Similarity 48.6%; Pred. No. 1.7e-24; 54; Conservative 16; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO compartible
OPERATUS SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: NO. 5955073 yet assigned
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAUNKESSEE: TOWNSEND AND TOWNSEND AND CLEW LIDE STREET: TWO EMbarcadero Center, Bighth Floor STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   015280-110310US
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APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-58F-1993
FILING DATE: 22-58F-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-DRR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/08891848
Patent No. 5955073
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Occyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 104 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 576-0300
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                                                                                                                          Best Local Similarity
Matches 54; Conserva
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Gaps

6

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1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
APPLICANT: Mikulski, Stanislaw M.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 104;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                              Query Match
45.6%; Score 274.5; DB 1;
Best Local Similarity 48.6%; Pred. No. 1.7e-24;
Matches 54; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19220728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERESTICS: LENGTH: 104 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/07921619
Patent No. 5595734
                                                                                                                                                                                                                            ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
          104 amino acids
                                                                                                                                                                              FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
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US-07-921-619-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "US-08-283-971-1

"Sequence 1, Application US/08283971

"Patent No. 5529775

"Sequence 1, Application US/08283971

"Patent No. 5529775

"SEQUENCE INFORMATION:

APPLICANT: Mikulski, Stanislaw M.

"ITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS

"ORRESPONDENCE ADDRESS:

ADDRESSE: Mark H. Jay, P.C.

"STREET: P.O. Box 020083, General Post Office

CITY: Brooklyn

"STATE: New York

CONNTR: New York

CONNTR: READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: PLOSS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 46.1%; Score 277.5; DB 3; Best Local Similarity 49.5%; Pred. No. 3.7e-24; Matches 55; Conservative 15; Mismatches 32;
            TILING DATE: 21-FBB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
RECISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECHMUNICATION INFORMATION:
TELEFEAX: (415) 576-0200
TELEFEAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LEGENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-198
FILING DATE: 06-APR-198
FILING DATE: 06-APR-198
FILING DATE: 10-APR-198
FILING DATE: 10-APR-198
FILING DATE: 13-NOV-1989
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
US 60/011,800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5006 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LECULARY: 718-V. TELEPHONE: 718-V. 718-625-0399
                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  US-08-875-811-43
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Floppy disk
MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Boix, Ester—
APPLICANT: Boix, Ardelt, Woleiech
TITLE OF INVENTION: A Matant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Prancisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.1%; Score 277.5; DB 4; Length 104; 49.5%; Pred. No. 7.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 63, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybac Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Widdwer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,429 FILING DATE: CLASSIFICATION: PAPLICATION PATA: APPLICATION: PAPLICATION PATA: APPLICATION NUMBER: 08/626,288 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEE: Townsend and Townsend and Crew LLP: Two Embarcadero Center, Eighth Floor San Francisco California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 15280-267
TELECOMOUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELERAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                  ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
  Wu, Yon-Neng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
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US-08-875-811-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-095-429-1
  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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1 QNWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 QDWLTFQKKHITNTRDVDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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; Sequence 43, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
    APPLICANT: Rybak, Susanna M.
    APPLICANT: Newton, Dianne L.
    APPLICANT: Newton, Dianne L.
    APPLICANT: Nodawer, Alexander
    TITLE OF INVENTION: Recombinant Ribonuclease Proteins
    NUMBER OF SEQUENCES: 64
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
46.1%; Score 277.5; DB 3; Length
Best Local Similarity 49.5%; Pred. No. 1e-24;
Matches 55; Conservative 15; Mismatches 32; Indels
                                        OFFRAINGS SYSTEM:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19-FEB-1998
CLASSIFICATION DATA:
FILING DATE: 19-FEB-1998
FILING DATE: 19-FEB-1998
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUBBAR: 41,739
REGISTRATION NUMBER: 41,739
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 129 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: TWO DRILLING.
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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Matches

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1 ONWAIFQORHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN
                                                               59 VLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                       59 VLSTTREQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wu, You-Neng
APPLICANT: Boix, Ester
APPLICANT: Boix, Dater
APPLICANT: Broix, Dater
APPLICANT: Ardelt, Wojeiech
TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
TITLE OF INVENTION: Allows Production by Recombinant Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105-1492
ZIP: 94105-1492
CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/626,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.1%; Score 277.5; DB 4;
49.5%; Pred. No. 7.7e-25;
iive 15; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 6649392 yet assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ran, David B.
REGISTRATION NUMBER: 38,589
REFERENCE/DOCKET NUMBER: 15280-267
TELECOMMUNICATION: (415) 543-9600
                                                                                                                                                                                                 ; Sequence 1, Application US/08626288
; Patent No. 6649392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09095429; Patent No. 6649393; GENERAL INFORMATION: APPLICANT: Youle, Richard
                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Youle, Richard
APPLICANT: Vasandani, Veena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Youle, Richard APPLICANT: Vasandani, Veena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Sar
STATE: Ca
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55;
                                                                                                                                                           RESULT 6
US-08-626-288-1
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US-09-095-429-1
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Best Local
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APPLICANT: Saxena, Shailendra K
APPLICANT: Saxena, Shailendra K
TITLE OF INVANTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REPERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
FRICR APPLICATION NUMBER: 09/394,268
FRICR APPLICATION NUMBER: 09/394,268
RIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                               1 ONWATFOOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ONWAIFQOKHIINI-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN 58
                                                                                                                                                         Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                         59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                               VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                             Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.1%; Score 277.5; DB 3; Length 104; 49.5%; Pred. No. 7.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 104;
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                                                                                               31, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32;
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                                                       Score 284.5; DB 1
Pred. No. 1.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.1%; Score 277.5; DB 4
49.5%; Pred. No. 7.7e-25;
iive 15; Mismatches 32
                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09687748 Patent No. 6423515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
Oocyte
                                                       47.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
                                                                                           55; Conservative
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rana pipiens
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Rana pipiens
US-09-394-268-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
Matches 55; Conserv
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US-08-467-955-2
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TYPE: PRT

SEQ ID NO 1

LENGTH:

Query Match

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Gaps

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Length 104; Indels 56

TYPE: PRT

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LENGIH:

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; OTHER INFORMATION: /note= "Frog Lectin from Rana; OTHER INFORMATION: catesbeiana"
US-08-875-811-8
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TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                       US-08-467-955-2; Sequence 2, Application US/08467955; Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
                                                                                         Query Match 97.8%;
Best Local Similarity 99.2%;
Matches 109; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jay, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            60 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                             97.8%; Score 588.5; DB 2; Length 111; 98.2%; Pred. No. 7.4e-61; tive 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Rybak, Susama M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SUGUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: DatentIn PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 19-FEB-1997
ATPLING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELLECOMMUNICATION NUMBER: 015280-244100US
                                                                                                                                /note= "Frog Lectin from Rana catesbeiana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco COUNTE: California COUNTEY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08875811; Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.23
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                           MOLECULE TYPE: protein FEATURE:
                                                                                                                     LOCATION: 1..111
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein LOCATION: 1..111
                                                                                                NAME/KEY: Protein
                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 94111-3834
             STRANDEDNESS:
                                                                                                                                                                                     US-08-891-848-12
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1 QNWAIFQQKHIINIPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 59
                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                 61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
Score 588.5; DB 3; Length 111; Pred. No. 7.4e-61; 1; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/178,118
PRILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
PRILING DATE: 13-NOV-1989
PRIOR APPLICATION NUMBER: US 07/814,332
PRIOR APPLICATION NUMBER: US 07/814,332
PRIOR APPLICATION NUMBER: US 08/81,970
PRILING DATE: 01-ROS-1994
PRILING DATE: 01-NOS-1994
PRILING DATE: 01-NOS-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/467,955 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATCATIN Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: 1
ORIGINAL SOURCE:
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ORGANISM: Rana pipiens

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GenCore version 5.1.6
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                Copyright
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OM protein - protein search, using sw model

7, 2004, 21:28:45 ; Search time 12.7596 Seconds (without alignments) 445.066 Million cell updates/sec Мау Run on:

602 1 QNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 US-09-961-400-15 Perfect score:

Scoring table:

Sequence:

389414 segs, 51625971 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

389414

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
7 cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/PcTuS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 12. Appl	α	'n	` -	Sequence 1. Appli		ì	9	43	Ì	ì	ì	13	39	4	51,			· -:	7	ı,	28.	30	3	ιG	5 6	4
SOMMAKIES	QI	US-08-891-848-12		-467-955-	-09-394-268	US-09-687-748-1	-288	429	-08-875-8	-08-875-			-08	-08-891-	US-08-875-811-39	8-875-	-875-	8-875-	9-394-268-	39-07	-09-687-748-	-09-98	US-08-875-811-28	875	-811-		-08-875-811-	US-08-875-811-49
	Length DB	111 2		104 1			104 4	104 4	129 3	379 3			104 1			m	m	Э	e	104 4	104 4	104 4	106 3	107 3	112 3	251 3	254 3	355 3
* Query	Match]	97.8	97.8	47.3	46.1	46.1	46.1	46.1	9	46.1	45.6	45.6	45.6	45.6	45.6	45.6	45.6	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3
	Score	588.5	588.5	284.5	277.5	277.5	277.5	277.5	277.5	277.5	274.5	274.5	274.5	274.5	274.5	274.5	274.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5
Result	No.	7	7	m	4	Ŋ	9	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

7. Appl			۸,	Appli	4. Appl		45. Appl			2. Appl	Appli	7. Appl	Appli	Appli	Appli	Annli	Appli
Seguence 57	Seguence 64			Sequence 2	Seguence 2	Sequence 26				100	ות	Seguence 4	Seguence 2	Sequence 1	Semience 4	Semience 2.	Sequence 3,
US-08-875-811-57	US-08-875-811-64	US-08-875-811-55	US-08-626-288-2	US-09-095-429-2	US-08-875-811-24	US-08-875-811-26	US-08-875-811-45	US-08-875-811-53	US-08-875-811-20	US-08-875-811-22	US-09-223-118-3	US-08-875-811-47	US-09-223-118-2	US-09-223-118-1	US-09-223-118-4	US-08-875-811-2	US-09-071-672-3
٣	m	٣	4	4	m	m	٣	ĸ	Э	e	m	m	m	m	e	m	4
355	355	366	104	104	105	105	358	365	107	111	114	360	114	114	114	83	83
45.3	45.3	45.3	44.8	44.8	44.4	44.4	43.8	43.8	41.4	39.8	39.2	37.8	37.7	37.5	37.4	34.2	34.2
272.5	272.5	272.5	269.5	269.5	267.5	267.5	263.5	263.5	249.5	239.5	236	227.5	227	226	225	206	206
28	59	3.0	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: TWO Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                   STREET: TWO Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: TWO Embarcadero Center, Eighth Floor
STREET: USA
COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION NUMBER: US 08/125,462
FILING DATE: US 08/125,462
FILING DATE: 2-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/14,082
FILING DATE: 2-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
APPLICATION NUMBER: US 07/510,696
FILING DATE: 22-OCT-1991
APPLICATION NUMBER: US 07/510,696
FILING DATE: 32-OCT-1991
ATTORNEY/AGRUT IRRORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                           ; Sequence 12, Application US/08891848; Patent No. 5955073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
US-08-891-848-12
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a synthetic ribonuclease protein, in

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/note= "this Gln is autocyclised to pyroglutamic acid"
                                                                                                                                                                                                                                                                          Amino acid sequence of a frog ribonuclease protein.
                                                                                                                                                                                                                                                                                    Frog; ribonuclease; ranpirnase; RNase
                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                          AAB31666 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                 99US-00394268.
                                                                                                                                                                                                                                                                                                                                                            99US-00394268
                                                                                                                                                                                                                                                               30-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                      (ALFA-) ALFACELL CORP
                                                                                                                                                    Sequence 104 AA;
                                                                                                                                                                                                                                                                                                         Key
Modified-site
                              04-APR-1997;
                                         04-APR-1996;
                                                                                                                                                                                                                                                                                              Rana pipiens
                                                                                                                                                                                                                                                                                                                             US6175003-B1
                                                                                                                                                                                                                                                                                                                                                 10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                            10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                       16-JAN-2001.
                    16-0CT-1997
                                                             Youle RJ,
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Saxena SK;

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New nucleic acids encoding a ribonuclease (Rnase), useful for the precise targeting of Rnase to a predetermined cell receptor.
                                                                                                                                                                                      The present sequence represents a frog ribonuclease protein (ranpirnase) (RNase). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targeting molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of ranpirnase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it might be most effective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: May 7, 2004, 21:38:28
Job time : 46.9224 secs
                                                                                                                                              Claim 1; Col 5-6; 7pp; English
                     WPI; 2001-167808/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55;
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Best Local
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a recombinant Onc protein comprising a 104 amino acid sequence having Gln at position 1. Onc, a ribonuclease from Rana pipiens occytes, is known as an antitumour agent (e.g. for treating pancreatic cancer) and inhibitor of human immunodeficiency virus type-1 replication. It can be used therapeutically or as a cell-culture selection agent, e.g. to identify gene therapy compositions able to inhibit tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant Onc protein with glutamine residue at position 1 - useful as antitumour and antiviral agent, also as cell culture selection agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ODWLIFOKKHIINTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQXPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                  Ardelt W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 277.5; DB 2;
; Pred. No. 8.3e-24;
15; Mismatches 32;
                                                                                                                                                                                                                                                                                                  Boix E,
                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                  Wu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 28; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.18;
                                                                                                                                              97WO-US005675.
                                                                                                                                                                                                96US-00626288
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Best Local Similarity 49.5'
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                  Vasandani VM,
                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-512725/47.
Rana pipiens
                                            WO9738112-A1
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                                                                                                                                        1 ONWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN
                                                                            Gaps
                                                                                                                                                                                           59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                  57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 104
                                                                          6
                                   46.1%; Score 277.5; DB 4; Length 104; 49.5%; Pred. No. 8.3e-24; ive 15; Mismatches 32; Indels 9;
                                                                          Conservative
                                                     Similarity
Sequence 104 AA;
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cancer; frog; autoimmune disease.

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The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met23Leu. Carboxy terminal end of recombinant RaPLRI has a dovalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytochoxic fusion proteins. They can be used for treatment of cancer and autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDWLTFQKKHLTNTRDVDCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 VLSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                        /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.3%; Score 278.5; DB 2
48.6%; Pred. No. 6.4e-24;
tive 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 34; Page 56; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY28869 standard; protein; 105
                                                                                                                                                                                                                                                                          99WO-US006641.
                                                                                                                                                                                                                                                                                                         98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
                                                        autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ08125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104 AA;
                                                                                                                                                      Misc-difference
                                                                                         Rana pipiens
                                                                                                                                                                                                                                                                        26-MAR-1999;
                                                                                                                                                                                                                                                                                                           27-MAR-1998;
                                                                                                                                                                                                       WO9950398-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000
                                                                                                                                                                                                                                       07-0CT-1999
                                                                                                         Synthetic.
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The present sequence is a recombinant Rana pipiens ribonuclease protein (RaPLRI) with Met at position 1 attached to (His)6 tag and Met24Leu. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties form expression proteins. They can be need for treatment of cancer and authorizants.
                                                                                                                                       note= "(His)6 histidine tag attached to N-terminal Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 ODWLTFOKKHLINTRDVDCNNILSTNLF --- HCKDKNTFIYSRPEPVKAICKGIIASKN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer; human immunodeficiency virus type-1; HIV1; replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 105;
                                                                                                              'note= "Met not found in wild type RaPLR1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                          /note= "Wild type Met replaced with Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.3%; Score 278.5; DB 2
48.6%; Pred. No. 6.5e-24;
iive 16; Mismatches 32
                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW30301 standard; protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 59; 71pp; English
                                                                                                                                                                                                                                                                        99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-610847/52.
N-PSDB; AAZ08127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 105 AA;
                                                                                            Misc-difference
                                                                                                                                                         Misc-difference
                             Rana pipiens.
Synthetic.
                                                                                                                                                                                                         WO9950398-A2
                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                      27-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                 Rybak SM,
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Kaposi's Sarcoma, human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

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gonadotrophin (hCg) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methicinine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
             Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi,'s sarcoma; human chorionic gonadotrophin; hGG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a recombinant Rana pipiens ribonuclease (RaPLRI) protein with Met at position 1. Carboxy terminal end of recombinant RaPLRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rana pipiens ribonuclease Clone 5alb; RaPLR1; covalently bound; RNase; LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ODWLTFOKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
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Pred. No. 2.9e-24;
5; Mismatches 32; Indels 9;
                                                                                                                                                                                                /note= "Met not found in wild type RaPLR1"
                                                                                                                                                                                                                                                                                                                                                                (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rana pipiens Clone 5alb ribonuclease.
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY28879 standard; protein; 127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 34; Page 57; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.8%;
                                                                                                                                                                                                                                                                                                99WO-US006641
                                                                                                                                                                                                                                                                                                                                 98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Rybak SM, Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                              autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ08126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 105 AA;
                                                                                                                                                                               Misc-difference
                                                                                                                Rana pipiens.
Synthetic.
                                                                                                                                                                                                                                                                                                26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25~JAN-2000
                                                                                                                                                                                                                                                                                                                                 27-MAR-1998;
                                                                                                                                                                                                                               WO9950398-A2
                                                                                                                                                                                                                                                                07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY28879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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The present sequence is a Rana pipiens clone 5alb ribonuclease (RapIRI). It is encoded by Clone 5alb cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncoase (RTM) at amino acid residues 11, 20, 85 and 103. Carboxy terminal end of RapIRI has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methicnine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonucleases allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ONWAIFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 ODWLÍFOKKHLTNIRDVDCNNIMSTNLF----HCKDKNIFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                       24. .127
/label= Rana_pipiens_Clone_5alb_ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant RaPLR1 Met23Leu amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.8%; Score 281.5; DB 2
49.5%; Pred. No. 3.7e-24;
cive 15; Mismatches 32
                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                        1. .23
/label= Signal_peptide
/note= "Putative"
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 69; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28866 standard; protein; 104 AA
                                                                                                                                                                                                                                                                    99WO-US006641.
                                                                                                                                                                                                                                                                                                    98US-0079751P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                 Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                             autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ08136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 127 AA;
                                                           Rana pipiens
                                                                                                                                                                                                                                                                    26-MAR-1999;
                                                                                                                                                                                                                                                                                                    27-MAR-1998;
                                                                                                                                                                                                       WO9950398-A2
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                                                                                                                                                                                                                                     07-0CT-1999
                                                                                                                                                                                                                                                                                                                                                                 Rybak SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY28866;
                                                                                                          Peptide
                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28866
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AAY28865 standard; protein; 104 AA.
                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        Newton DL;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-610847/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAZ08124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 104 AA;
                                                                                                                                                                                                                                  Rana pipiens
                                                                                                                                                                                                                                                            WC9950398-A2
                                                                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                               27-MAR-1998;
                                                                                                                                                                                                                                                                                       07-OCT-1999.
                                                                                                      25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
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                                                                                                                                                                                                                                                                                                                                                                                                        SM,
                                                                        AAY28865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY28867;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        Rybak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                  AAY28865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY28867
                 RESULT
                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW6543) that have been isolated from Rana pipiens occytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy and surgery in the treatment of tumours
                                                                                                                 59
                                                                                                                                     ENWATFQQKHINTPINCNTIMDNNIYIVGQQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
(Rana catesbelana) lectin used to describe the method of the invention
                                                                                                                1 QNWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ONWATFOOKHIINT-PIICNTIMDNNIYIVGGCCKRVNTFIISSATTVKAICTGVI-NMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDWLTFOKKHVTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                       LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
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                                                           Length 111;
                                                                                                                                                                                           LSTIRFQLNTCTRISITPRPCPYSSRIBINYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antitumour proteins from Rana pipiens oocyte(s) - have fewer disadvantages than chemotherapy, surgery and radiotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                       Indels
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49.5%; Pred. No. 1.3e-24;
ive 16; Mismatches 31;
                                                           DB 2;
                                                        Score 588.5; DB 2
Pred. No. 2.2e-59;
                                                                                                                                                                                                                                                                                                                                                        Antitumour protein from Rana pipiens oocytes.
                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Tumour; chemotherapy; radiotherapy; frog.
                                                                                                                                                                                                                                                                       AAW06544 standard; protein; 104 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 28; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-00467955.
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                                                        97.8%;
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Best Local Similarity 49.58
Matches 55; Conservative
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ALFA-) ALFACELL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-043063/04.
                                                                     Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 104 AA;
                             Sequence 111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Rana pipiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ardelt WJ;
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                                                        Query Match
                                                                                                                                                                                                                                           RESULT 8
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                                                        Rana pipiens liver ribonuclease, RaPLR1; covalently bound; LL2 antibody, ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog; human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase; signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant ribonucleases, used for killing target cells, treating cancers, viral infections or autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.8%; Score 281.5; DB 2
49.5%; Pred. No. 2.9e-24;
ive 15; Mismatches 32
Rana pipiens liver ribonuclease (RaPLR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 55; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US006641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0079751P.
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Length 111;

110

The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6 tag, MetZiBeu and MetSiBeu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (RG) effective against Kaposi's sarcoma calls. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1; recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease. ONWATEQOKAIINTPIICNTILDNNIYIVGGQCKRUNTFIISSATTVKAICTGVINLNVL 60 note= "(His)6 histidine tag attached to N-terminal Met" ONWATFQOKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60 New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases. STIRFOLNICIRISIIPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein. STIRFQLNICIRISITPRPCPYSSRIEINYICVKCENOYPVHFAGIGRCP 'note= "Met not found in wild type RaCOR1" 'note= "Wild type Met replaced with Leu" /note= "Wild type Met replaced with Leu" (USSH) US DEPT HEALTH & HUMAN SERVICES Location/Qualifiers Claim 22; Page 66; 71pp; English. AAY28876 standard; protein; 111 99WO-US006641. 98US-0079751P. (first entry) Rybak SM, Newton DL; WPI; 1999-610847/52. catesbeiana N-PSDB; AAZ08133 Misc-difference Misc-difference Misc-difference Misc-difference 27-MAR-1998; WO9950398-A2 25-JAN-2000 07-0CT-1999 Synthetic AAY28876; Н 61 Rana RESULT 6 g 용 Š

Sequence 111 AA;

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This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cyperising surface marker on be used for selectively killing cells cytotoxic agent. The products can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1. Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepaticis viruses (B, non-A-non-B, and delta), herpes zoster. Cytomegalovirus) and cells infected with parasites (such as the malaria parasite)). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation in throby selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow calls in box selectively can also be used as carrow) prior to transplantation into a patient undergoing marrow calls in the patient of the killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a bullfrog
                                      ·:
                                                                                                            2 QNWATFQOKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVL 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy chain; cell surface marker; treatment; tumor; viral infection; parasite infection; immune dysfunctional cell; autoimmune disease; contraceptive; cell separation; transplantation; bone marrow ablation; leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
                                                                            QNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
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                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nntly fused pancreatic RNase-targeting proteins useful for tumors, infections, immune or autoimmune disorders and as
                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
                                                                                                                                                                          STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                        STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                                        ·.
                                        Indels
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99.0%; Score 596; DB 2; 98.2%; Pred. No. 3e-60; ive 2; Mismatches
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                                                                                                                                                                                                                                                                                          AAY33321 standard; protein; 111
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91US-00779195.
93US-00014082.
93US-00125462.
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                                      Conservative
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                    108; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                        Recombinant Met (-1) Rana catesbeiana occyte ribonuclease Gln1Ser; RacOR1, coadaently bound: LL2 antibody, ligand binding moiety; cancerous B cell; Kaposi, s sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
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                                                                                        NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                                              NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
                                   Gaps
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                                                                                                                             TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
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                                   Indels
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                                                                                                                                                                                                                                                                                                                                          Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
Pred. No. 2.3e-60;
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                                                                                                                                                                                                                                           AAY28878 standard; protein; 111 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         CD22; RNase; autoimmune disease
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             100.0%;
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               Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana catesbeiana.
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Length 111;

99.2%; Score 597; DB 2; I 100.0%; Pred. No. 2.3e-60;

Query Match Best Local Similarity

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                                                                                                                       62
                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; RaCORI Met22Leu Met57Leu; LLZ antibody; ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.
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                                                                                                                    3 NWAIFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
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Pred. No. 3e-60;
2; Mismatches 0;
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109; Conservative
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Matches 108, Conservative
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Length 111;

Score 602; DB 2; Pred. No. 6.2e-61;

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                                                                 Matches 110; Conservative
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Best Local Similarity
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 Sequence 111 AA;
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cytotoxic fusion proteins. They can be used for treatment of cancer and
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                                                                                Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Met not found in wild type RaCOR1"
                                                                                                                  0; Indels
                                                                                100.0%; Score 602; DB 2; 100.0%; Pred. No. 6.1e-61;
                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        AAY28873 standard; protein; 111 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 22; Page 63; 71pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Met(-1) RaCOR1
                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                  Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-610847/52.
N-PSDB; AAZ08131.
                autoimmune diseases
                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rana catesbeiana.
                                                 Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9950398-A2
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                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000
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                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                          AAY28873;
                                                                                Query Match
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The present sequence is a recombinant Rana catesbeiana oocyte recombinant RaCOR1) protein with Gln16er. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadorrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an Neterminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytocoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases
                                                                                                                                                                                                                             Recombinant Rana catesbeiana oocyte ribonuclease; RacOR1 Gln1Ser; CD22; covalently bound; LL2 antibody; ligand binding moiety, cancerous B cell; bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase; signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant ribonucleases, used for killing target cells, e.g. treating cancers, viral infections or autoimmune diseases.
/note= "Wild type Gln replaced with Ser"
                                                                                                                                                                                                 Recombinant RaCOR1 Gln1Ser amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 67; 71pp; English.
                                                                                             AAY28877 standard; protein; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0079751P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US006641
                                                                                                                                                                                                                                                                                                    cancer; autoimmune disease.
                                                                                                                                                                  entry)
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                                                                                                                                                                (first
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Length 110;

5

DB

Score 597;

99.2%;

Query Match

autoimmune diseases

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                     Copyright
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- protein search, using sw model OM protein

May :uo Run

7, 2004, 21:25:55 ; Search time 46.9224 Seconds (without alignments) 662.376 Million cell updates/sec

US-09-961-400-15

602 1 ONWAIFQOKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1586107 seqs, 282547505 residues Searched:

1586107

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

A_Geneseq_29Jan04:* Database

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2001s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	
SUMMARIES		CE00CX & & C OVE O OOL COU
	DB	C
	Length	6,1
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	sult Query No. Score Match Length DB ID	000
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Result No.	Score	Query Match	Length	DB	ID	Description
ч	602	100.0	110	2	AAY28872	Aay28872 Rana cate
N	602	100.0	111	7	AAY28873	3 Recom
ო	597	99.2	110	C)	AAY28877	_
4	597	99.5	111	C)	AAY28878	00
S	596	99.0	110	(1	AAY28874	4
9	596	0.66	111	7	AAY28876	9
7	88.		111	7	AAY33321	
80	284.5	47.3	104	N	AAW06544	4
6	81.	46.8	104	7	AAY28865	
10		46.8	105	7	AAY28867	~
11	281.5		127	0	AAY28879	6
12	278.5	46.3	104	7	AAY28866	9
13	278.5	46.3	105	7	AAY28869	
	277.5	46.1	104	7	AAW30301	Aaw30301 Recombina
15	277.5	46.1	104	4	AAB31666	
16	277.5	46.1	104	Ŋ	ABG32650	Abg32650 Northern
17	277.5	46.1	105	N	AAY39400	
18	277.5	46.1	379	7	AAW35126	Aaw35126 R. pipien
19		45.9	1	ď	AAY28870	Aay28870 Recômbina
20	76.	45.9	105	0	AAY28871	Aay28871 Recombina
21	74.	45.6	104	(1	AAR12344	44
22	274.5		104	7	AAR47303	Aar47303 ONCONASE
23	74.		104	N	AAW00736	Aaw00736 Protein d
24	274.5	45.6	104	7	AAW14065	Aaw14065 Onconase
25	274.5	45.6	104	7	AAW06543	

Aaw88233 Rana pipi Aay33322 Frog onco	Aaw35123 R. pipien Aaw35125 R. pipien	Aaw35130 R. pipien Aab31667 Amino aci		Aaw35122 R. pipien Aaw35117 R. nipien	Aaw35118 R. pipien	Aaw35134 R. pipien	Aaw35135 R. pipien	Aaw35133 R. pipien	Aaw35129 R. pipien	Aaw35132 R. pipien	Aaw30302 Recombina	Aaw18224 Antitumou	Aaw35115 R. pipien	Aaw35116 R. pipien	Aaw35127 R. pipien
AAW88233 AAY33322	AAW35123 AAW35125	AAW35130 AAB31667	ABG31617	AAW35122 AAW35117	AAW35118	AAW35134	AAW35135	AAW35133	AAW35129	AAW35132	AAW30302	AAW18224	AAW35115	AAW35116	AAW35127
77	0 0	C/ 4	S.	7 7	7	7	7	ď	2	N	~	7	7	0	~
104	105 355	358 104	104	106	112	251	254	355	355	366	104	104	105	105	358
. N	45.6 45.6	45.6 45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.3	45.1	44.4	44.4	44.4	43.8
274.5	274.5	274.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	272.5	271.5	267.5	267.5	267.5	263.5
	28 29	30 31	32	3 3	35	36	37	38	39	40	41	42		44	45

ALIGNMENTS

Rana catesbeiana oocyte ribonuclease, RaCOR1; covalently bound; CD22; L2 antibody; Ligand binding molety, cancerous B cell; Raposi's Sarcoma; human chorionic gonadotrophin; hG3: recombinant ribonuclease; bullfrog; signal peptide; cytotoxic fusion protein; cancer; autoimmne disease; Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence. AAY28872 standard; protein; 110 AA (first entry) 25-JAN-2000 AAY29872; RESULT 1 AAY28872

Rana catesbeiana. Synthetic.

W09950398-A2

07-OCT-1999.

99WO-US006641. 98US-0079751P 26-MAR-1999; 27-MAR-1998; (USSH) US DEPT HEALTH & HUMAN SERVICES.

Newton DL; Rybak SM,

WFI; 1999-610847/52. N-PSDB; AAZ08130.

New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 62; 71pp; English.

The present sequence is a Rana catesbeiana oocyte ribonuclease (Racori) protein encoded by a cDNA modified for expression in B. coli. Carboxy terminal end of Racori has a covalently bound ligand binding moiety, which can be a LLZ antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hGG) effective against Raposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form

us-09-961-400-13.rsp

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                                                                                                                                                                                                                                                                                                                                                                                         20.5%; Score 119.5; DB 1; Length 145; 30.8%; Pred. No. 6.5e-06; ative 12; Mismatches 45; Indels 17; Gaps
                                                          R EMBL; U22516; AAA91366.1; -.
R EMBL; U22516; AAA91366.1; -.
R EMBL; BC055355; AAH55555.1; -.
R HSRP; P03950; 1A4.
R HSRP; P03950; 1A4.
R InterPro; IPR001427; RNaseA.
R PRINTS; PR00794; RIBONUCLEASE.
R PRODOM; PD000535; RNaseA; 1.
SWART; SW00092; RNASe Pc; 1.
R PROSTTE; PS00127; RNASE Pc; 1.
R PROSTTE; PS00127; RNASE Pc; 1.
R Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                             ANGIOGENIN.
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                  06944260BB764938 CRC64;
                                                                                                                                                                                                                                                                                                                                                                  16228 MW;
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Best Local Similarity 30.89
Matches 33; Conservative
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145
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64
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104
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145 AA;
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ACT_SITE
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DISULFID
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SEQUENCE
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Search completed: May 7, 2004, 21:53:05 Job time : 5.30402 secs

58 V-LITSEFYLSDCNVTS----RPCKYKLKKSINTFCVTCENQAPVHF 99

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                                                                                                                     IASKNVL------TTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--AP 96
                                                                                           SDWLTFQKKHL-----INTRDVDCNNIM---SINLFHCKDKNTFIYSRPEPVKAICKGI
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Echimyidae; Proechimys.
NCBI_TaxID=10163;
                                                               30; Gaps
                                                                                                                                                                                                                                                                                                                                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.6%; Score 120; DB 1; Length 128; 29.9%; Pred. No. 5e-06;
                                            20.6%; Score 120; DB 1; Length 128; 28.5%; Pred. No. 5e-06; tive 21; Mismatches 37; Indels
                                                                                                                                                                                                                                         01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
02-RDB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKED (GLCNAC. . .).
2DB58093A9D3C936 CRC64;
                          A2F4101A1A33E93B CRC64;
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein.
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BY SIMILARITY.
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                                                                                                                                                                                                                          128 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Nuclease; Endonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 BN 95 BN 110 BN 12 BN 141 BN 1424 MW N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P00656; ISRN.
InterPro: IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRIWTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                         Proechimys guairae (Casiragua)
21
34 N.
64 L
14406 MW;
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58
65
12
41
119
34
128 AA;
21
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64
128 AA;
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                                              Query Match
Best Local Similarity
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CARBOHYD
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                            SEQUENCE
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          CARBOHYD
CARBOHYD
                   VARIANT
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RNP PROGU
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7 FOKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STAIN=FVHON'N; ISSUE=Liver;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A placken M., Soares M.B., Bonaldo M.F., Carvin E.M., Hong L.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Bosak S.A., McEwan P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Holdon D.K., Munny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Munny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Munny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

Rabesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Dickson M.C.,

Rab Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schmetch A., Schein J.E., Jones S.J.M., Marra M.R.;

"Generation and initial analysis of more than 15,000 full-length

Fig. Thuman and mouse cDNN sequences.";
Biochim. Biophys. Acta 1162:177-186(1993).

-!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
-!- function the surface of endothelial cells; once bound,
angiogenin is endocytosed and translocated to the nucleus, thereby
promoting the endothelial invasiveness necessary for blood vessel
formation. Angiogenin induces vascularization of normal and
malignant tissues. Abolishes protein synthesis by specifically
                                                                                                       64 PCKNGQSNCYESTSNWHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPUHF 120
                                                                        59 -----LTTSEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                    01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIJNE=91025023; PubMed=2222458;
Bond M.D., Vallee B.L.;
"Isolation and sequencing of mouse angiogenin DNA.";
Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 LIFOKKHLINIRDVD-----CNNIMSINLF---HCKDKNIFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 NVLCKNGRINCYESNSTMHITDCRQTGSSKYPNCAVKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVL------TTSEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Biol. Evol. 19:438-445(2002).

-!-FUNCTION: May function as a tRNA-specific ribonuclease that binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endothelial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang J., Rosenberg H.F., "Diversifying selection of the tumor-growth promoter angiogenin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
                                                                                                                                                                                                                                                                                                                                                                                               Length 124;
                                                                                                                                                                                                                                                                                                                          76 N-LINKED (GLCNAC, . .) (30%).
14125 MW; F57475459F697B20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           42; Indels
InterPro; IPkuul,

Pfam; PF00074; rnaseA; 1.

R PRUTS; PR00794; RIBONUCLEASE.

R PTDIOM; PD000535; RNaseA; 1.

R SMART; SM00092; RNASe Pc; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.

KWART; SM00127; RNASE PANCREATIC; 1.

R PGSITE; PS00127; RNASE PANCREATIC; 1.

R PATCOLASE; Bndonuclease; Glycoprotein.

AM Hydrolase; Nuclease; Endonuclease; Glycoprotein.

R PATCOLASE; RNASE PANCREATIC; 1.

R PROSITE; PS00127; RNASE PS00127; 
                                                                                                                                                                                                                                                                                                                                                                                                               Pred No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                               Score 125; DB 1;
                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
                                                                                                                                                                                                                                                                                SIMILARITY
SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21918422; PubMed=11919285;
                                                                                                                                                                      BY
BY
BY
BY
BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF441667; AAL61649.1: -
                                                                                                                                                                                                                                                                                                                                                                                               21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Macaca.
                                                                                                                                                                      84
95
110
72
12
41
                                                                                                                                                                                                                                                                                                                                                   124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primate evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                              41
119
76
                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANGI MACMU
Q8WN63;
                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
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                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                ACT SITE
                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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PRINTS; PR00794; RIBONUCLEASE.

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                                                                                                                                                                                                                                                                                                                                                    6 TFQKKHLINIRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIC---KGIIASKNV-LIT
                                                                                                                                                                                                                                                                                                     23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pancreas;
MEDLINE=77185022; PubMed=862624;
Van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,
Beintema J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure and glycosidation.";
Eur. J. Blochem. 75:91-100(1977).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphacliponucleotides ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
ProDom; Pubuses, Masse Pe; 1.
RARATE, SMO0092; RNASE PARCHEATIC; 1.
RHOSITE; PSO0127; RNASE PARCHEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Frotein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
SIGNAL 97 146 ANGIOGENIN.
24 ANGIOGENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 41, Last sequence update)
Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
Cavia porcellus (Guinae pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                        PYRROLLIONE CARBOXYLIC ACID (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                      Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the pancreatic ribonuclease family. PIR; A00826; NRGPB.
                                                                                                                                                                                                                                                                            .5,
4e-06;
-hes 32; Indels
                                                                                                                                                                                                                                       E39A89215DB2A2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    98 SPFQVTTCKLRGGSPRPPCQYRATRGSRNIVVGCENGLPVH 138
                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                                                                                                                                                                                                                                                                                                                          62 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH
                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Nuclease; Endomolease; Glycoprotein.

DISULFID 40 95 BY SIMILARITY.

DISULFID 58 110 BY SIMILARITY.

DISULFID 65 72 BY SIMILARITY.

ACT_SITE 12 BY SIMILARITY.

ACT_SITE 11 BY SIMILARITY.

ACT_SITE 11 BY SIMILARITY.

ACT_SITE 11 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 AA
                                                                                                                                                                                                                                                                    20.9%; Score 121.5;
                                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P00656; IGRN.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; P0000535; RNaseA; 1.
SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANNEATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                     Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- TISSUE SPECIFICITY: Pancreas.
                                                                                                                                                                                                                                    16301 MW;
                                                                                                                                                                                                                                                                                     28.78;
                                                                                                                                                                                                                                                                                 Local Similarity 28.7%
les 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                       37
64
138
105
116
131
                                                                                                                                                                                      50 1
63 1
81 1
146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAVPO
                                                                                                                                       ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
                                                                                                                                                                                                 DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                   Query Match
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7 FOKKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 FERQHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 L-----TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF 99
TISSUE=Pancreas;
MEDLINE=7705676, PubMed=999896;
MEDLINE=7705676, van den Hende-Timmer L., Beintema J.J.;
"Isolation, properties and primary structure of coypu and chinchilla pancreatic ribonuclease.";
Biochim. Biophys. Acta 453:400-409(1976).
-!- CATALYIIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphotaes and 3'-phosphotoligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emmens M., Welling G.W., Beintema J.J., "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blochem. J. 157:317-323 (1976).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphates and 3-phosphooligonucleotides ending in C-P or with 2',3'-cyclic phosphate intermediates.
-!- SUBCELULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                       -i- TISSUE SPECIFICITY: Pancreas.
-i- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
RNASE1 OR RNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LINKED (GLCNAC. . .).
4EB924E52B445832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | PROSILE; | PROULE; | ANADOL | PROSILE; | P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 1;
1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.6%; Score 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANCREATIC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=76277855; PubMed=962870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 BY
195 BY
110 BY
72 BY
12 BY
141 BY
34 N-
14267 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P00656; 1SRN.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASe Pc; 1
PROSITE; PS00127; RNASE_PAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity 29.9
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00074; rnaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A00822; NRCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribonuclease.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P00673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DATO DE LA PARTA LA P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
            δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                  resonance spectroscopy,";
Biochemistry 35:8870-8880(1996).
Biochemistry 35:8870-8880(1996).
Lenderistry 35:8870-8880(1996).
Lo actin on the surface of endothelial cells; once bound angiogenin is endocytosed and translocated to the nucleus, thereby promoting the endocytosed and translocated to the nucleus, thereby promoting the endochtolial invasiveness necessary for blood vessel formation. Angiogenin induces vascularization of normal and mailgnant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular triNAs. Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity.
Li SUBCELLULIAR LOCATION: Secreted.
LI TISSUE SPECIFICITY: Serum and milk.
LI SINIARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVDCNNIMSTNLF--HCKDKNTFIYSRPEPVKAICKGIIASKN------VLTTSEFYL
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Mammalia; Butheria; Rodentia; Hystricognathi; Myocastoridae;
            "Solution structure of bovine angiogenin by 1H nuclear magnetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.0%; Score 128; DB 1; Length 148; 34.0%; Pred. No. 8.3e-07; ive 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16969 MW; B7999124CBB523DD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWART; SM00092; RNAse_Pc; 1.
POSSTE; PS00127; RNASE_PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 SDC---NVTSR-PCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myocastor coypus (Coypu) (Nutria).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001427; RNaseA.
PEdm; PE00074; TraseA. 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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PDB; 1GIO; 07-DEC-96.
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ACT_SITE ACT_SITE

SIGNAL CHAIN

DISULFID DISULFID PIR; A00818; NRWHK HSSP; P00656; 1SRN

NCBI_TaxID=10157;

Myocastor [1] SEQUENCE.

RNP_MYOCO

1D RNP M

AC 21-JU

DT 21-JU

RNASE

OC MAMMA

RNP_MYOCO P00676;

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Query Match SEQUENCE

63

Gaps

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36; Indels

Length 128;

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Chang S.-I.;
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T primate evolution...

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                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                        --- PCKYKLKKS
                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; lrnuseA; 1.
Pfam; PF00074; maseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
PRODON; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protecin synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                         ; Score 130.5; DB 1; Length 145; Pred. No. 4.4e-07; 11; Mismatches 29; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5)
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PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                           31 CKDKNTFIYSRPEPVKAIC--KGIIASKNV-LITSEFYLSDCNVTSR
                                                                                                                                                              // SIMILARITY.
29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 AA.
                                                                    SIMILARITY
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MEDLINE=21918422; PubMed=11919285;
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                                                                                                                                                                                        16612 MW;
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                                                                                                                                                                                                                                                         22.4%;
38.2%;
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                                                                                                                                                                                                                                                                                                                    Conservative
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ACT_SITE
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MOD RES
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61
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                                                                                                                                                        6 TFQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPBPVKAIC---KGIIASKNV-LTT
                                                                                                                                  23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A., "The complete amino acid sequence of bovine milk angiogenin."; FEBS Lett. 241:41-45(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bond M.D., Vallee B.L.; "Isolation of bovine angiogenin using a placental ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95224057; PubMed=7708754; Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.; Crystal structure of bovine anglogenin at 1.5-A resolution."; Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
                                                                                                          Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and expression of bovine angiogenin."; to the EMBL/GenBank/DDBJ databases.
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MEDLINE=96280645; PubMed=8688423;
Lequin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
                                                                                                                                   Indels
                                                                             27860112E85B8DF9 CRC64;
                                                                                                                                                                                                                               98
                                                                                                                                                                                                             62 SEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVH
                                                                                                         DB 1;
                                                                                                                                  17; Mismatches 30;
                                                                                                                     4.4e-07;
                                                                                                                                                                                                                                                                                                ANGI BOVIN
P10152; Q9GKP9;
01-MAR-1989 (Rel. 10, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
- wnp-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bond M.D., Strydom D.J.;
"Amino acid sequence of bovine angiogenin.";
Blochemistry 28:6110-6113(1989).
                                     SIMILARITY.
SIMILARITY.
SIMILARITY.
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             SIMILARITY
                                                                                                        Score 130.5;
Pred. No. 4.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89065101; PubMed=3197838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor binding assay.";
Biochemistry 27:6282-6287(1988).
                                                                               16444 MW;
                                                                                                      22.4%;
                                                                                                     Query Match
Best Local Similarity 30.7*
Matches 31; Conservative
37
64
138
105
116
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Submitted (MAR-1999) t
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146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IISSUE=Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rissum=Liver;
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STANDARD;
84
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110
72
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411
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                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                             124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 PVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 PVHF 99
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ID ANGR MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beintema J.J., Neuteboom B.;

"Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives:

"Origin of the duplicated ribonuclease.";

J. Mol. Evol. 19:145-152(1983).

-! - CATALYTIC ACTIVITY: Endomucleolytic cleavage to nucleoside 3'-

-! PATALYTIC ACTIVITY: Endomucleolytic cleavage to nucleoside 3'-

-! SURGELULIAR LOCATION: Secreted.

-! SUBCELULIAR LOCATION: Secreted.

-! TISSUE SPECIFICITY: Pancreas.

-! SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                  Prodom; Predomoclease; Priorididone carboxylic acid.

M Hydrolase; Nuclease; Endomoclease; Prirolidone carboxylic acid.

M Hydrolase; Nuclease; Prirolidone carboxylic acid.

M Hydrolase; N
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2', 3'-cyclic phosphate intermediates.
-!- STBCIELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; 541111.
HSSP: P00656; 1LSQ.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 THYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRIACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 IIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Galea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%; Score 144; DB 1; Length 119; 30.1%; Pred. No. 1.3e-08; ive 19; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87036770; PubMed=6571219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                    Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Galea musteloides (Cuis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A00827; NRUI.
HSSP; P00656; 1SRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNP_GALMU
P00680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDWLIFQKKGHL-----INTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKG 51
                                                                                                                                                                                                                                                                                                                                                                                                       3 SSAMKFOROHMDSDGHPDTNTN--YCNEMNVRRSMTOGRCKPVNTFVHEPLEAVOAVC-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 IIASKNV-----LITISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCEN--QA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRALH=129, TISSUE-Liver;
STRALH=129, TISSUE-Liver;
MEDLINE=56079109; PubMed=8530072;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
Brown W.E., Nobile V., Subramanian V., Shapiro R.;
"The mouse angiogenin gene family: structures of an angiogenin-related genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                          MISSING (IN 1/3 OF THE MOLECULES) 609C7E251A7BBA25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANGIOGENIN-RELATED PROTEIN. PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                        22.7%; Score 132; DB 1; Length 124; 30.6%; Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                                                           36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R Pfam; PF00074; rnaseA; 1

R PRINTS; PR00794; rnaseA; 1

R PRINTS; PR00794; RLBONUCLEASE.

SMART; SM00092; RNAse Pc; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

Signal; Hydrolase; Nuclease; Endonuclease;

Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 AA.
SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                            SIMILARITY.
                                                                                                                                                                                                                                                                                                         18; Mismatches
                                                                           SIMILARITY
                                                                                                      SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Angiogenin-related protein precursor.
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  BY
BY
BY
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BY
                                                                                                                                                                                                       13870 MW;
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MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U22519; AAA91367.1; -.
                                                                                                                                                                                                                                                                                                              38; Conservative
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RNP IGUIG
P80287;
                                                                                               SEOUENCE
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                                                                                                                                                          liver."
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      28
                        82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DWLTFOKKHLINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV
             J. Biochem. 108:139-143(1990).
-!- FWOVTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.
-!- SUBGELIULAR LOCATION: Secreted.
-!- SUBCILIULAR LOCATION: Secreted.
-!- STATIARRIP: Belongs to the pancreatic ribonuclease family.
PIR: JX0120: JX0120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                  Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
"Amino acid sequence of a lectin from Japanese frog (Rana japonica)
                                                                                                                             01-NOV.1990 (Rel. 16, Created)
01-FBB-1994 (Rel. 28, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Sialic acid-binding lectin (EC 3.1.27.-).
Bukaryotica (Japanese reddish frog):
Bukaryotica, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia; Anura, Neobatrachia; Ranoidea; Rana.
                                        59 LTISEFYLSDC---NVISRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LITSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.2%; Score 280.5; DB 1; Length 111; 44.5%; Pred. No. 3.1e-23; Live 19; Mismatches 35; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNAŠE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                111 AA.
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                                                                                                               PRT;
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                                                                                                                                                                                                                                         MEDLINE=91035319; PubMed=2229005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY
BY
                                                                                                                                                                                                                         AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 44.5%;
Conservative 1
                                                                                                               STANDARD;
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35
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82
97
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34
52
94
111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                TISSUE=Egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNPL RANCA
ID RNPL RANCA
AC P14626;
                                                                                                               RANJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                    24
                                                                                                                                                                                                                       SEQUENCE,
                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
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                                                                                                                       P18839;
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Matches
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3 DWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKNV 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE
                                                                                                                                                                                                                                                                                              Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y., Okazaki T., Ohgi K., Irie M., "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                             J. Blochem. 106:729-735(1989).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphateintermediates ending in C-P or U-P
with 2',3'-cyclic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; JX0085; JX0085.
InterPro; IPR001427; RNaseA.
                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iguana iguana (Common iguana).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana.
NCBI_TaxID=8517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00127; RNASE PANCHEATIC; 1.

Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

MCD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

ACT_SITE 10 BY SIMILARITY.

ACT_SITE 104 104 BY SIMILARITY.

DISULFID 19 72 BY SIMILARITY.

DISULFID 34 BY SIMILARITY.

DISULFID 52 97 BY SIMILARITY.

DISULFID 94 111 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 LITSEFYLSDC---NVTSRPCKYXLKKSTNIFCVICENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao W., Beintema J.J., Hofsteenge J.;
"The amino acid sequence of iguana (Iguana iguana) pancreatic
ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Created)
1-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Elbonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.4%; Score 264.5; DB 1;
42.7%; Pred. No. 1.6e-21;
ive 19; Mismatches 37;
01-APR-1990 (Rel. 14, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Edonuclease, liver (EC 3.1.27.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                          MEDLINE=90130374; PubMed=2613682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 219:641-646(1994)
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MEDLINE=94139745; PubMed=8307028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12461 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Conservative
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Best Local Similarity
                                                                                                                                                                              NCBI_TaxID=8400;
                                                                                                                                                                                                                                                     TISSUE=Liver;
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2;

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54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
62
                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                  RNPO_RANCA STANDARD; PRT; 133 AA.
P11916, Q9PWR7;
01-0CT-1989 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-2003 (Rel. 42, Last annotation update)
Elbonuclease, oocytes precursor (BC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
                                                                                                                                                                                             3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                    DWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIŜSUB-EGG;
MEDLINE-87299649; PubMed-3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Takayanagi G., Hakomori S.;
"Amino acid sequence of sialic acid binding lectin from frog (Rana
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98165825; PubMed=9497370;
Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
Huang H.C., Wang a createsbelana rcr gene encoding a cytotoxic ribonuclease.
Tissue distribution, cloning, purification, cytotoxicity, and active
residues for Rhase activity.";
J. Biol. Chem. 273:6395-6401(1998).
                                                                                                                                                                                                                                                                                                                                                Rana catesbeiana (Bull frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                             .;
0
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                                                                                                                                                            Score 551; DB 1; Length 104;
Pred. No. 3.9e-52;
                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                            EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                     11845 MW; 22A753C2F9E566B4 CRC64;
                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION, AND SEQUENCE OF 81-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A pyrimidine-guanine sequence-specific
catesbeiana (bullfrog) oocytes.";
Nucleic Acids Res. 20:1371-1377(1992).
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92220613; PubMed=1373237;
Liao Y.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catesbeiana) eggs.";
Biochemistry 26:2189-2194(1987).
                                                                                                                                                             94.78;
                                                                                                                                                                     96.1%;
                                                                                                                                                                             Conservative
SEQUENCE OF 23-133.
                                                                                                                                              104 AA;
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8400;
                66;
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DISULFID
DISULFID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
Chang cartesbelana structure of a cyctoxic ribonuclease from the occytes
of Rana catesbelana (bullfrog) ";
J. Mol. Biol. 283:231-244(1998)";
-!-FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
-!-FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
as substrates, and prefers the former. The S-lectins in frog eggs
may be involved in the fertilization and development of the frog
embryo. This lectin agglutinates various animal cells, including
normal lymphocytes, erythrocytes, and fibroblasts of animal and
human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMATT; SW00092; KNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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8
TISSUE=Egg;
MEDLINE=93192604; PubMed=8448385;
Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Nitta K., Oyama F., Itani K.;
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of sialic acid-binding lectin from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the pancreatic ribonuclease family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID.
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Signal; Pyrrolidone carboxylic acid.
SIGNAL

CHAIN

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ACT_SITE

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DISULPID

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SUBCELLULAR LOCATION: Secreted.
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PIR; AZ7121; AZ7121.
PDB; 1BC4; 28-OCT-98.
PDB; 1M07; 21-JAN-03.
INTERPRO; IPR001427; RNASEA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNASEA; 1.
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                                                                                                                                                                                                                                                                                                                     Glycobiology 3:37-45(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 23-133
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122
133 AA;
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                                                                                                                                                                                                                                                                         catesbeiana eggs.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 21:30:40; Search time 5.30402 Seconds (without alignments) 1030.796 Million cell updates/sec May Run on:

US-09-961-400-13 582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 141681 segs, 52070155 residues Searched:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	neinin ener 93020G		rana		iguan	galea	8 mus mu	cerc		เก	~	~	P00679 cavia porce	proech	_	Q8wn64 papio hamad	D	. ,	P31347 oryctolagus	Ln	a		homo	Q8wme8 pan troglod	mus	P00671 sus scrofa	hyst		Q9wus1 myoxus glis	P34096 homo sapien	eduns	Q8wn60 saimiri sci	_
SUMMARIES	ΩI	RN30 RANPI	RNPO_RANCA	LECS RANJA	RNPL_RANCA	RNP IGUIG	RNP GALMU	ANGE MOUSE	ANGI CERAE	ANGI BOVIN	RNP MYOCO	RNP_BALAC		RNPB CAVPO	RNP PROGU	ANGI MOUSE	ANGI PAPHA	RNP CHIBR	RNP_HYDHY	ANGI RABIT	ANGI MIOTA	RNP HIPAM	RNS4 PANTR	ANGI_HUMAN	ANGI PANTR	ECP3 MOUSE		RNP_HYSCR	RNP BOVIN	RNP MYOGL	RNS4 HUMAN	RNP HORSE	ANGI SAISC	RNBR_BOVIN
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ماره	Query		49.3	48.2	2	4	22.7	22.4	22.4			21.5			20.6	0				19.9						o,		•	19.2			19.1	19.1	19.1
	Score	551	287	280.5	264.5	144	132	130.5	130.5	128	126	125	121.5	120		119.5	118.5	118	117	116	115		113.5	113	113	113	112	112	112	_	111.5	111	111	111
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P31346 sus scrofa	POOSTS CAVIA POICE	V2954z giraira cam O8wn62 saquinus oe	P87350 axis porcin	P97425 mus musculu	P80929 bos taurus	P07847 aepyceros m	P00668 antilocapra	P00661 ovis aries	046529 saimiri sci
ANGI PIG	RNPA_CAVPO	ANGI SAGOE	RNBR AXIPR	ECP2_MOUSE	ANG2_BOVIN	RNP AEPME	RNP ANTAM	RNP_SHEEP	RNS6_SAISC
ч.			Ч	Н	Н	Н	Н	Н	Н
123	124	146	151	156	123	124	124	124	150
19.0	18.9	18.9	18.9	18.9	18.7	18.7	18.7	18.7	18.6
110.5	110	110	110	110	109	109	109	109	108.5
ю и 4 п	36	38	39	40	41	42	43	44	45

ALIGNMENTS

RRSUND ACCOOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	RANPI RANPI RANPI RANPI RANPI RANPI RED-1991 (Rel. 11-FAGE-1991 (Rel. 13-15-100-100-100-100-100-100-100-100-100-	randard; 19, Created 11, Last as 12, Ar 12, Ar 12, Ar 12, Ar 13, Last ar 14, Ar 16, Last as 16, Last as 17, Ar 18, Last ar 18, Last ar 18, Last ar 18, Last ar 19, Last ar 10, Last ar 11, Last ar 12, Last ar 12, Last ar 13, Last ar 14, Last ar 15, Last ar 16, Last ar 17, Last ar 18, Last ar 18	PRT; iduance u motation motation motation deficit eobatrac gen K.; gen K.; delt umor mology t. 91). 177; delt w., delt	pdate) pdate) update) update) a; Vertebrata; Haia; Ranoidea; Haia; Ranoidea; Haia; Ranoidea; Haia; Ranoidea; Haia; Ranoidea; Hains ocytes and tens ocytes and serivity."; cactivity.";	a; Euteleostomi; a; Ranidae; Rana. n Rana pipiens ribonucleases."; 4., Shogen K., on of P-30 protein. and early and early an i-f-ycytotoxic activit well as antitumor rity against high : blastomere stage) .ease family.
	To e	To m	To m	To m	SULT. 1 30_RANPI 92_069. 92_069. 92_069. 92_069. 92_069. 92_069. 93_069. 94_061. 95_108. 95_108. 96_108. 96_108. 96_108. 96_109. 96

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                                                                                                                                                                                                                                                                                                                             53 IASKNVLTT----SEFYLSDCNVTSR----PCKYKLKKSTNTFCVTCENQ--APVHF 99
                                                                                                                                                                  20; Gaps
                                                                                                       Query Match

20.1%; Score 117; DB 1; Length 128;
Best Local Similarity 28.0%; Pred. No. 0.00011;
Matches 33; Conservative 21; Mismatches 44; Indels
C;Keywords: hydrolase; nucleic acid digestion; pancreas F;12,41,119/Active site: His, Lys, His #status predicted F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
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anglogenin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29833; B43825
B;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186; 1993
A;Title: Characterization and Sequencing of rabbit, pig and mouse angiogenins: discernme A;Reference number: S29833
A;Title: Characterization and Sequencing of rabbit, pig and mouse angiogenins: discernme A;Reference number: S29833
A;Accession: S29833
A;A

Gaps 8, Query Match
Best Local Similarity 31.2%; Pred. No. 0.00013;
Matches 24; Conservative 13; Mismatches 32; Indels 31 CKDKNTFIYSRPEPVKAICK---GIIASKNV-LTTSEFYLSDCNVTS----RPCKYKLKK 82

à g à dd

83 STNTFCVTCENQAPVHF 99

99 GSRNIVIAČENGLPVHF 115

Search completed: May 7, 2004, 21:54:54 Job time: 9.5276 secs

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A, Molecule type: protein
                                                                                                                                                    Query Match
Best Local Similarity
Matches 33; Conserv
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Bur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancratic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID:77185023; PMID:862624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues C; Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NyAlternate names: angiogenesis factor
NyAlternate names: angiogenesis factor
CySpecies: Mus musculus (house mouse)
CySpecies: Mus musculus (house mouse)
CyAccession: A35932
Ry Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-955, 1990
A;Title: Isolation and sequencing of mouse angiogenin DNA.
A;Reference number: A35932; MuID:91025023; PMID:2222458
A;Accession: A35932
A;Status: not compared with conceptual translation
A;Reiden: DNA
A;Residues: 1-145 < BON>
A;Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:g726326
C;Genetics:
A;Introns: #status absent
C;Function:
A;Description: hydrolyzes tRNA; induces vascularization of normal and malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
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                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
                                                                                                                                                                                              64 PCKNGQSNCYESTSNWHITDCRLTSNSKFPDCLYRTSQEEKSIIVACEGNPYVPVHF 120
                                                                                                                           8 PORQHIDSSGSPSTNPNYCNAMMKSRNMTQERCKPVNTFVHEPLADVQAVC----FQKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 SDWLTFOKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISEFYLSDCNVTSRP----CKYKLKKSINTFCVTCENQ--AP
                                                                                   7 FQKKHL-----INTRDVDCNNIM-SINLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                            Gaps
                                                                                                                                                                                                                                                                                                                          B - guinea pig (tentative sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein, hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His Lys, His #status predicted
F;21,44/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                      -LITSEFYLSDCNVTSR----PCKYKLKKSINTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                          28;
    Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
20.6%; Score 120; DB 1;
29.9%; Pred. No. 5.3e-05;
iive 18; Mismatches 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.6%; Score 120; DB 1;
28.5%; Pred. No. 5.3e-05;
iive 21; Mismatches 37
                                                                                                                                                                                                                                                                                                                        pancreatic ribonuclease (EC 3.1.27.5) N/Alternate names: RNase IB
                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-128 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 35; Conserv
                    Best Local Similarity
Matches 35; Conser
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    Query Match
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Fil-24/Domain: signal sequence #status predicted <SIG>
Fi25-145/Product: anglogenin #status predicted <MAT>
Fi25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;37,64,137/Active site: His, Lys, His #status predicted
F;50-104,63-115,81-130/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 guinea-pig: comparison of the amin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rivan den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Blochys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic A;Reference number: A90612; MUID:77065676; PMID:999896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic ribonuclease (EC 3.1.27.5) - Chinchilla brevicaudata (tentative sequence) NiAlternate names: RNase 1, RNase A C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000 C;Accession: A00820
C;Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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NyAlternate names: RNase 1; RNase A
C;Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C;Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C;Accession: A00824
R;Beintema, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A;Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparisc A;Reference number: A92957; MUID:87036770; PMID:6571219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 FQKNVPCKNGQSNCYQSNSNMHITDCRLTSNSKYPNCSYRTSRENKGIIVACEGNPYVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KFLTQHHDAKPKGRDDRYCERMMKRRSLTSPCKDVNTFIHGNKSNIKAICGANGSPYREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SDWLTFQKKHL----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAICKGII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SSAMKFOROHDSSGSPSTINANYCNEMMKGRNMTQGYCKPVNTFVHEPLADVQAVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --LITSEFYLSDCNVISRP----CKYKLKKSINTFCVICENQ--APV
                                                                                                                                                                                                                                                                                                                                                                                         -CNNIMSTNLF--HCKDKNTFIYSRPEPVKAIC--KGIIASKN
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12-41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                                            DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-124 <VAN>
A;Note: a second component of chinchilla ribonuclease has 32-Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 V-LITSEFYLSDCNVTS----RPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                         20.5%; Score 119.5; DB 1
30.8%; Pred. No. 6.8e-05;
iive 12; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 118; DB 1; 27.0%; Pred. No. 8.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A00824
A;Molecule type: protein
Residues: 1-128 <BEL>
C;Superfamily: pancreatic ribonuclease
                                                                                                                                                                                                                                                                                                                   33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                         10 KHLTNTRDVD---
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7; 28 63

Gaps

28;

99

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C; Accession: A00818
B; Emmens, M.; Welling, G.W.; Beintema, J.J.
Bicochem. J. 157, 311-323, 1976
A; Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease A; Reference number: A00818; MUID:76277855; PMID:962870
A; Accession: A00818
A; Accession: A008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 LTFQKKHLTNTRDVD-----CNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||
|VLCKNGRINCYESNSIWHITDCRQIGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LCKNGQINCYQSNSNMHITDCRVTSNSDYPNCSYRTSQEEKSIVVACEGNPYVPVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N,Alternate names: RNase 1; RNase A
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorgual)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FOXKHL-----TNTRDVDCNNIM-STNLF--HCKDKNTFIYSRPEPVKAICKGIIASKNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 FERQHMDSRGSPSTNPNYCNEMMKSRNMTQGRCKPVNTFVHEPLADVQAVC----FQKNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 NVL-------TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TISEFYLSDCNVTSRP----CKYKLKKSTNTFCVTCENQ--APVHF
                                                                                                                                                                             F;26-84,40-95,58-110,65-72/Disulfide DOMUS: #Status processing F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                       acid digestion; pancreas
                                                                                                                                                                                                                                                                                                                                                                 Length 128;
           C;Superfamily: pancreatic ribonuclease
C;Reywords: glycoprotein; hydrolase; nucleic acid digestion; g
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                           Query Match 21.6%; Score 126; DB 1; L. Best Local Similarity 29.9%; Pred. No. 1.3e-05; Matches 35; Conservative 18; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.5%; Score 125; DB 1; 28.6%; Pred. No. 1.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreatic ribonuclease (EC 3.1.27.5) - minke whale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches
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Best Local Similarity
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R/Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A/Title: Crystal structure of bovine angiogenin at 1.5 Angstroms resolution.
A/Reference number: A58315; MUID:95224057; PMID:7708754
A/Contents: annotation; C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
R/Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
A/Contents: annotation; conformation by (1)H-NMR, residues 1-125
R/Lequin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Blochemistry 35, 8870-8880, 1996
A/Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance spec A/Reference number: A5881; MUID:96280645; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280645; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280647; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280647; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280647; PMID:8688423
A/Contents: annotation; conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280647; PMID:8688423
A/Contents: Annotation; Conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280647; PMID:8688423
A/Contents: Annotation; Conformation by (1)H-NMR
R/Reference number: A58921; MUID:96280647; PMID:8688423
A/Contents: Annotation; Conformation by (1)H-NMR
R/Reference number: A5994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coypu and chinchilla pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ġ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 DEYCENMMKNRRITRPCKDRNTFIHGNKNDIKAICE----DRNGQPYRGDLRISKSEFQI 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    C.; Montreuil, J.; Spik, G.; Tartar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                         A, Experimental source: plasma
R, Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar
FEBS Lett. 241, 41-45, 1988
A, Title: The complete amino acid sequence of bovine milk angiogenin.
A, Reference number: S02001; MUID:89065101; PMID:3197838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.0%; Score 128; DB 1; Length 125; 34.0%; Pred. No. 8.2e-06; Live 14; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C) Superfamily: paracreatic ribonuclease
C) Keywords: angiogenesis; hydrolase; nucleic acid degradation
E;60-68/Region: receptor binding #status predicted
F;14,41,115/Active site: His, Ly8, His #status predicted
F;27-82,40-93,58-108/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J. Biochim. Biophys. Acta 453, 400-409, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: milk R; Riordan, J.F.; Vallee, B.L. R;Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L. submitted to the Brookhaven Protein Data Bank, January 1995 A; Reference number: A65065; PDB:1AGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: Isolation, properties and primary structure of
A,Reference number: A90612; MUD:77065676; PMID:999896
A,Accession: A00822
A,Molecule type: protein
                                                           A, Title: Amino acid sequence of bovine angiogenin.
A, Reference number: A32474; MUID: 89375344; PMID: 2775757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHF
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ochemistry 28, 6110-6113, 1989
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Best Local Similarity 34.08
Matches 33; Conservative
                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-125 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein A; Residues: 1-125 < MAE>
                                                                                                                                                                             A; Accession: A32474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S02001
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Pancreatic ribonuclease (EC 3.1.27.5) - cuis
NyAlternate names: RNase 1; RNase A
C'Species: Galea mustabloides (cuis)
C'Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C'Accession: A00827
R'Beintema, U.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
J. Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amir A; Reference number: A92957; MUD:87036770; PMID:6571219
A; Reference number: A92957; MUD:87036770; PMID:6571219
A; Residues: 1-124 - GBIY
A; Residues: 1-124 - GBIY
A; Robert one-third of the molecules lacked Ala-1
C; Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
C; Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
C; Superfamily: pancreatic ribonuclease
C; Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
C; Superfamily: pancreatic ribonuclease
C; Comment: The cuis is a rodent belonging to the same subfamily as the guinea pig.
C; Superfamily: A1,119/Active site: His Lys, His #status predicted
F; 26-84,40-95,58-110,65-72/Pisulfide bonds: #status predicted
F; 26-84,40-95,58-110,65-72/Pisulfide bonds: #status predicted
F; 94/Binding site: carbohydrate (Asn) (covalent) #status absent
C;Species: Iguana iguana (common iguana)
C;Date: 19-War-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Bur. J. Biochem. 219, 641-646, 1994
A;Fitle: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenin [validated] - bovine
NyAlternate names: angiogenesis factor
NyContains: ribonuclease (EC 3.1.27.
C.Species: Bos primigenius taurus (cattle)
C.Species: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 15-Sep-2000
C.Accession: A32474; S02001; A30044; S48212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 DWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEPVKAIC--KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 SDWLTFQKKHL-----TNTRDVDCNNIM---STNLFHCKDKNTFIYSRPEFVKAICKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 THYEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPGTKRIRLACENNQPVHF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 IIASKNVLTTSE-FYLSDC----NVTSRPCKYKLKKSTNTFCVTCENQAPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                       24.7%; Score 144; DB 2;
30.1%; Pred. No. 1.9e-07;
ive 19; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.7%; Score 132; DB 1; 30.6%; Pred. No. 3.2e-06; iive 18; Mismatches 36
                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: protein
A:Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease
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30.6%; Pic.
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34; Conservative 1
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les 38; Conserv
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                                                                                                                                                                                                                        A; Accession: S41111
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C; Species: Rana catesbeiana (bullfrog)
C; Species: Rana catesbeiana (bullfrog)
C; Species: Rana catesbeiana (bullfrog)
C; Species: On-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C; Accession: JX0085
R; Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A; Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A; Reference number: JX0085; MUID: 90130374; PMID: 2613682
A; Accession: JX0085
A; Accession: JX0085
A; Mulp: pancreatic ribonuclease
C; Reywords: hydrolase; pyroglutamic acid (Gln) #status experimental
F; J, Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; J, Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F; J, Accession: JX04 Active site: His, Lya, His #status predicted
                                                                                                                                                                                                                                            ribonuclease-related stalic acid-binding lectin - Japanese frog
C;Species: Rana japonica (Japanese frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JX0120
R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawauchi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                             LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENGYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 LITSEFYLSDC---NVTSRPCKYKLKKSINIFCVICENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Readues: 1-11 < KAM-
A; Resperimental source: egg
C; Superfamily: pancreatic ribonuclease
C; Superfamily: pancreatic ribonuclease
C; Keywords: lectin; pyroglutamic acid
F; I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; I/Modified site: 97,94-111/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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48.2%; Score 280.5; DB 1;
Best Local Similarity 44.5%; Pred. No. 3.6e-21;
Matches 49; Conservative 19; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
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Matches
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RESULT 841111

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 7, 2004, 21:38:36; Search time 9.5276 Seconds (without alignments) 1060.090 Million cell updates/sec

US-09-961-400-13 582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ribonuclease-relat	se	ribonuclease-relat	pancreatic ribonuc				- 14	pancreatic ribonuc				• • • •		angiogenin - rabbi			pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	pancreatic ribonuc	ribonuclease 4 (EC	ribonuclease - dom	pancreatic ribonuc	pancreatic-type ri	angiogenin - pig	•	pancreatic ribonuc	
SUMMARIES	מו	A39035	A27121	JX0120	JX0085	841111	NRUI	A32474	NRCU	NRWHK	NRKS	NRGPB	A35932	NRCB	NRYY	B43825	NRHP	NRHUAG	NRBOB	NRPG	NRPQ	NRBO	I52489	S08549	NRHO	\$20066	A43825	JC6159	NRGPA	JC6160
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	% Query Match	94.7	49.3	48.2	45.4	24.7	22.7	22.0	21.6	21.5	20.6	20.6	20.5	20.3	20.1	19.9	19.6	19.4	19.2	19.2	19.2	19.2	19.2	19.1	19.1	19.1	19.0	19.0	18.9	18.9
	Score	551	287	280.5	9	144	132	128	126	125	120	120	119.5	118	117	116	114	113	112	112	112	112	111.5	111	111	111	110.5	110.5	110	110
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NRSH	NRPRH	S07141	NRWB	NRGN	NRGF	NRDEO	NRCM	NRCMM	NRCMB	NROW2	NRHY	NRDER	NRDEN	NREKN	NRDEF
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124	124	124	124	124	124	124	124	124	124	128	124	124	124	124	124
18.7	18.7	18.7	18.6	18.6	18.4	18.0	18.0	18.0	18.0	18.0	17.9	17.7	17.7	17.7	17.5
109	109	109	108	108	107	105	105	105	105	105	104	103	103	103	102

ALIGNMENTS

 RESULT 1 A39035 ribonuclease-relate C;Species: Rana pip C;Date: 31-Jul-1991 C;Accession: A39035 K;Ardelt, W.; Mikul J; Biol: Chem. 266, A;Title: Amino acid A;Reference number: A;Accession: A39035 A;Status: prelimina	RESULT 1 A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment) Syspecies: Rana pipiens (northern leopard frog) C,Species: Rana pipiens (northern leopard frog) C,Speciesion: A39035 E,Accession: A39035 A,Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and eax A;Reference number: A39035; MUD:91093131; PMID:1985896 A,Stacession: A39035 A,Status: preliminary
 A;Molecule ty, A;Residues: 1 C;Superfamily Query Match Best Local Matches 9	A;Nolecule type: protein A;Residues: 1-104 cARD> C;Superfamily: pancreatic ribonuclease C;Superfamily: pancreatic ribonuclease Best Local Similarity 96.1%; Pred. No. 2.5e-48; Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 op Q	3 DWLIFQKKHLINIRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Qy Db	63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
RESULT 2 A27121 ribonuclease-relate C;Species: Rana cat C;bate: 19-Nov-1988 C;Accession: A27121 R;Titani, K.; Takio Biochemistry 26, 21 A;Title: Amino acid A;Reference number: A;Accession: A27121 A;Residues: 1-111 C;Superfamily: panc C;Keywords: lectin	RESULT 2 ribonuclease-related sialic acid-binding lectin - bullfrog C;Species: Rana catesbeiana (bullfrog) C;Species: Rana catesbeiana (bullfrog) C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993 C;Accession: A27121 B;Itlani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawauchi, H.; Takayanag B;Itle: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana) A;Hclesrence number: A27121; MUID:87299649; PMID:3304421 A;Accession: A27121 A;Residues: 1-111 cTIT> C;Superfamily: pancreatic ribonuclease C;Keywords: lectin
Query Mat Best Loca Matches	Query Match Best Local Similarity 49.1%; Pred. No. 8.1e-22; Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;
 à d	3 DWLTFQKKHLINTRDVDCNNIMSTNLFHCKDRYFFIYSRPEPVKAICKGIIASKNV 58 :

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Search completed: May 7, 2004, 21:51:57 Job time : 33.6904 secs

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; Sequence 8, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-948-391A-8
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                            3 DWLTPQKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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APPLICANT: Newton, Dianne U.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
TITLE REPLANT: Department of Health and Human Services
TITLE REPERENCE: 015280-3431100/S
TITLE REPERENCE: 015280-3431100/S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 1998-03-26
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                           96.9%; Score 564; DB 10;
99.0%; Pred. No. 4.4e-57;
live 0; Mismatches 1;
                                                                                                                                                                                                              ; OTHER INFORMATION: ribonuclease (RaPLR1)
US-09-948-391A-2
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: NewFon, Dianne L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.0°
Matches 102; Conservative
                                                                                                                                                                       ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                    TYPE: PRT
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RESULT 14 US-09-961-400-4

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Sequence 4, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANA M.
APPLICANT: RYBAK, SUSANA M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
FILE REPERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 DWLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEDVKAICKGIIASKNVLTTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 36.9%; Score 564; DB 10; Length 104; al Similarity 98.1%; Pred. No. 4.4e-57; 101; Conservative 1; Mismatches 1; Indels
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APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne D.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: bepartment of Health and Human Services
TILE REPERENCE: 015280-341100S
CURRENT APPLICATION NUMBER: US (09/948,391A
CURRENT APPLICATION NUMBER: US (0/079,751
PRIOR APPLICATION NUMBER: W 60/079,751
PRIOR APPLICATION NUMBER: W 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1090-03-16
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/62,61,400
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1000-08-17
PRIOR PLILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
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PRIOR PLILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING PARE: PAGENTIN VET: 2.1
SEQ ID NOS: 43
PROFIWARE: PAGENTIN VET: 2.1
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; ORGANISM: Rana pipiens
US-09-961-400-28
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US-09-948-391A-2
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| Publication No. US20030124131A1
| GENERAL INPORMATION:
| APPLICANT: RYBAK, SUSANNA M.
| APPLICANT: RYBAK, DAVID M.
| APPLICANT: GOLDENBERG, DAVID M.
| APPLICANT: MEWYON, DIANNE L.
| TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: UNMBER. US/09/961,400
| TITLE OF INVENTION: UNMBER: 09/622,613
| FILE REPERENCE: 2001-09-25
| CURRENT FILING DATE: 2000-08-17
| PRIOR FILING DATE: 2000-08-17
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1999-03-26
| PRIOR FILING DATE: 1998-03-26
| NUMBER OF SEQ ID NOS: 43
| SOFTWARE: PATCHIN VOE: 2.1
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OTHER INFORMATION: insert
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  EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                  EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-00-27
PRIOR PILING DATE: 1998-00-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
SPRIOR FILING DATE: 2000-08-17
SOFTWARE: PATENTING NUMBER: US 09/622,613
                                                                                                                                                                                            Sequence 28, Application US/09948391A
Publication No. US20030027311A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Rana pipiens
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US-09-961-400-28
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: 108733/1059
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR PELLORION NUMBER: 90/622,613
PRIOR PELLORION NUMBER: PCT/US99/06641
PRIOR PELLORION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
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PRIOR FILING DAT
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                             Length 127;
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APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311005
                                  Score 573; DB 10;
Pred. No. 5.1e-58;
CURRENT APPLICATION NUMBER: US/09/948,391A CURRENT FILING DATE: 2002-05-10 PRIOR APPLICATION NUMBER: US 60/079,751 PRIOR FILING DATE: 1998-03-27 PRIOR APPLICATION NUMBER: WO PCT/US99/06641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09961400; Publication No. US20030124131A1; GENERAL INFORMATION:
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Best Local Similarity 96.2
Matches 101; Conservative
                             Query Match 98.5
Best Local Similarity 100.
Matches 103; Conservative
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ORGANISM: Rana pipiens
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1; Mismatches
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CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: US/09/961,400
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 07/US99/06641
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATCHIN VET: 2.1
                  Sequence 9, Application US/09961400
                                     Publication No. US20030124131A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.1%;
Matches 103; Conservative
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ORGANISM: Rana pipiens
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US-09-961-400-2
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Best Local Similarity
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Best Local Similarity
Matches 103; Conserv
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Publication No. US20030124131A1

GENERAL INPORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: RYBAK, SUSANNA M.

TITLE OF INVENTION: DIANNE L.

TITLE OF INVENTION: CELLS

FILE REFERENCE: 019733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: PCT/US99/06641

FRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SOFFWARE: PREFETTION OF: 21

SOFFWARE: PREFETTION OF: 21
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                                                                                                                                                                                                                                                                   FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:Rana pipiens;
CTHER INFORMATION: ribonuclease with Gln1Ser substitution
CHER INFORMATION: (recombinant RaPLR1 Q1S)
US-09-948-391A-11
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99.1%; Score 577; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 104; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 104
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Rana pipiens
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US-09-961-400-11
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RESULT 7 US-09-961-400-9

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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR PILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 9
TENNING NOS: 43
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; Sequence 2, Application US/09961400
; Sequence 2, Deplication US/09961400
; Publication No. US20030124131A1
; Publication No. US20030124131A1
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NGMIDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ISEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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Pred. No. 2.6e-58;
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RESULT 5
US-09-948-391A-11
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REPREBACE: 108793/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALCHING UNC: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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                                                                               TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 002-05-10
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PILING DATE: 1099-03-26
PRIOR PILING DATE: 1000-08-17
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
                                                                                                                                                                                                        US-09-961-400-13
; Sequence 13, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Rana pipiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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LENGTH: 105
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APPLICANT: MINCACATION:
APPLICANT: MINCACATION:
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TAPLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TILE OF INVENTION: CELLS
TILE OF INVENTION: CELLS
TILE OF INVENTION: CELLS
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR PRILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: ECT/US99/06641
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
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OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant; CTHER INFORMATION: Met(-1) RapLR1)
US-09-948-391A-6
                                                                                                                                                       Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 105;
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Pred. No. 1.1e-58;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         publication No. Consume M. GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M. APPLICANT: Rybak, Dianne L. APPLICANT: The Worton, Dianne L. APPLICANT: The United States of America APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services ITILE OF INVENTION: Recombinant Anti-Tumor RNase; TITLE OF INVENTION: NUMBER: US/09/948,391A
                                                                                                                                                       99.3%; Score 578; DB 10;
99.0%; Pred. No. 1.1e-58;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.0%;
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                        Best Local Similarity 99.0
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Rana pipiens
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2004, 21:29:40 ; Search time 33.6904 Seconds (without alignments) 865.070 Million cell updates/sec May Run on:

US-09-961-400-13 582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Perfect score:

Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

1140673 segs, 277566755 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database

PUDLIBRIED APPLICATIONS AND AND ADDRESS.

(SGNZ_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

(SGNZ_6/ptodata/2/pubpaa/US07 BW PUB.pep:*

(SGNZ_6/ptodata/2/pubpaa/US06 BW PUB.pep:*

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(SGNZ_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:* Published_Applications_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 13, Appl	13,	9	. 9	11	11,				28,		Sequence 2, Appli	4	4	80
	Š.	1.0	US-09-948-391A-13	US-09-961-400-13	US-09-948-391A-6	US-09-961-400-6	US-09-948-391A-11	US-09-961-400-11	US-09-961-400-9	US-09-961-400-2	US-09-948-391A-28	US-09-961-400-28	US-09-961-400-8	US-09-948-391A-2	US-09-948-391A-4	US~09-961-400-4	US-09-948-391A-8
			10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	1	datch bength DB	105	105	105	105	104	104	111	104	127	127	105	104	104	104	105
ď	Query	March	100.0	100.0	89.3	99.3	99.1	99.1	98.8	98.5	98.5	98.5	97.1	96.9	6.96	96.9	96.2
	i c	SCOLE	582	582	578	578	577	577	575	573	573	573	565	564	564	564	260
	Result	- PAC-	1	7	m	4	ഗ	9	7	80	6	10	11	12	13	14	15

Sequence 9, Appli	7	1, 1	·~i	53	ω,	Sequence 3, Appli	· vo	26,	Sequence 17, Appl	24,	24,	Sequence 21, Appl	21,	22,	Sequence 22, Appl	15,	15,	Sequence 17, Appl	19	19	ď	89	139	5		G	N	2	Seguence 254, App
10 US-09-948-391A-9	14 US-10-153-882-2	9 US-09-986-119-1	10 US-09-918-887-1	12 US-10-461-713-53	9 US-09-986-119-3	10 US-09-918-887-3	10 US-09-948-391A-26	10 US-09-961-400-26	10 US-09-961-400-17	10 US-09-948-391A-24	10 US-09-961-400-24		10 US-09-961-400-21		10 US-09-961-400-22	10 US-09-948-391A-15	10 US-09-961-400-15		10 US-09-961-400-19	an	us	12 US-10-016-248-89	15 US-10-074-978A-139	13 US-10-016-447-5		9 US-09-286-240-6	9 US-09-863-777-2	9 US-09-731-872-254	10 US-09-876-997-254
111	105	104	104	104	83	83	111	111	111	110	110	111	111	117	117	110	110	111		110			119	===	124	147	147	147	147
96.2	95.5	94.7	94.7	93.3	76.5	76.5	49.1	49.1	48.4	48.2	48.2	47.7	47.7	47.7	47.7	47.5	47.5	47.3	46.8	45.8	27.1	24.7	24.7	22.1	21.5	19.4	19.4	19.4	19.4
260	256	551	551	543	445	445	285.5	285.5	281.5	280.5	280.5	277.5	277.5	277.5	277.5	276.5	276.5	275.5	272.5	266.5	157.5	144	144	128.5	125	113	113	113	113
16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens; OTHER INFORMATION: Tibonuclease with Met at position 1 and Gln2Ser; CTHER INFORMATION: substitution (recombinant Met (-1) RaPLR1 Q1S) US-09-948-31A-13
Sequence 13, Application US/09948391A
Fublication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: NPAAK, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311008
FILE REFERENCE: 015280-34311008
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
FRIOR PRILING DATE: 1998-03-27
FRIOR PILING DATE: 1998-03-26
FRIOR APPLICATION NUMBER: WO PCT/US99/06641
FRIOR APPLICATION NUMBER: WO 967/US99/06641
FRIOR PILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1050-08-17
WUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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Gaps . 0 100.0%; Score 582; DB 10; Length 105; llarity 100.0%; Pred. No. 3.7e-59; Conservative 0; Mismatches 0; Indels 0; Query Match Best Local Similarity Matches 105; Conservat

0

1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIXSRPEPVKALCKGIIASKNVLT

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0; Gaps
                                                                                                                                                                                                                                                                       Query Match

Best Local Similarity 96.1%; Pred. No. 1.5e-59;
Matches 99; Conservative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INPORMATION FOR SEQ ID No: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
HYPOTHETICAL: N
ANTI-SENSE: N
PRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
CORGANISM: Rana pipiens
US-08-467-955-1
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Search completed: May 7, 2004, 21:40:44 Job time: 12.1796 secs

Gaps

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2 DWLIFPQKKHITNIRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKALCKGIIASKNVLITS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Mark H. Jay, P.A.
STREET: P.O. BOX E
CITY: Short Hills
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

94.7%; Score 551; DB 1;

Best Local Similarity 96.1%; Pred. No. 1.5e-59;

Matches 99; Conservative 2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-APR-1988
FRICA APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FBB-1992
FRIJNG DATE: 01-ABS-1992
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/467,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PCT_DOS/MS_DOS SOFTWARE: Patentin Release #1.24 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,95: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 5007 US TELECOMMUNICATION INFORMATION: 201-912-9066
           TELEPRIONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5556734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE FRARACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jay, Mark H. REGISTRATION NUMBER: 27507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONTINX: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          N-terminal
                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                           ANTI-SENSE: N
FRAGMENT TYPE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                  TOPOLOGY:
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US-08-467-955-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 DWLIFOKKHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Mojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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CURRESPONDENCE ADDRESS:
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 06-APR-1988
PRICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY AGENT INFORMATION:
ANAMER TAREST AND ADTA:
ANAMER TAREST AND AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 551; DB 1;
Pred. No. 1.5e-59;
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REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: 424, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPRAN: 718-625-0399
TELERX: No. 5529775 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5595734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.1%;
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: N
                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-283-971-1
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APPLICATION NUMBER: US 07/436,141
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Pred. No. 1.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rybar, Susanna M.
APPLICANT: Rybar, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Lluis
APPLICANT: Windawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
STATE: California
COUNTRY: USA
APPLICANT: Wlodawer, Alexander
TITTLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                     COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PAPELICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRICK APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAILS, SUBBRE 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
MUMERATION NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
MUMERATION NUMBER: 015280-244100US
                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-875-811-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                         ZIP: 94111-3834
                                                                                                                                                                                                    USA
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                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
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1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFTYSRPEPVKAICKGIIASKNVLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Ardelt Ph.D, Wojciech J.
APPLICANT: Mixuliski, Stanislaw M.
TITLE OF INVENTION: PHERMACEUTICAL FOR TREATING TUMORS IN HUMANS NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 555; DB 3;
Pred. No. 5e-60;
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUL-1992
UMBER: US 07/178,118
06-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-283-971-1; Sequence 1, Application US/08283971; Patent No. 5529775
                                                                                                                                                                                                                                                                                                                                                  NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.2
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-875-811-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-JUI APPLICATION NUMBER:
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61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
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                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94111.3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                       Sequence 41, Application US/08875811
Patent No. 6045793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 51, Application US/08875811; Patent No. 6045793; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Faris, Susan K.
REGIZERATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01.
FELECOMMUNICATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 355 amino acids
amino acid
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                             STREET: TWO EMEGACISTICS SAN Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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US-08-875-811-51
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEDWLTFQKKHITNTROVDCDNINSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
                                                                                                                                                                 2 DWLTFQKKHVINITRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                                                 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS
                                                                                                   Gaps
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                                                            Length 104;
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                                                      Score 556; DB 1; Length 10
Pred. No. 3.7e-60;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                  63 EFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94111.3834

COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPATE: DatentIN Release #1.0, Version #1.30
SOFTWARE: PatentIN BATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
FILING APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1997
FILING DATE: 12-FEB-1997
FILING DATE: 12-FEB-1997
FILING DATE: 21-FEB-1996
ATTOMNEY/AGRAFI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Bighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 556; DB 3;
Pred. No. 3.8e-60;
2; Mismatches 3;
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  Oocyte
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REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INPERMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                    Query Match

Best Local Similarity 97.1%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.5%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-875-811-39
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 100; Conserv
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                                                                                                                                                                                                                                                                                                                           US-08-875-811-39
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  us-08-467-955-2
                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Widdwer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION 5435
PRIOR APPLICATION DATA:
APPLICATION 1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INPORMATION:
NAME: Faris, Susan K.
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LL:
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.5%; Score 556; DB 3;
95.2%; Pred. No. 1.8e-59;
iive 2; Mismatches 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rybak, Susanna M.
Newton, Dianne L.
Boque, Lluis
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 5007 UN TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELETAX: 201-912-0465
TELETAX: No. 5728805 Applicable INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-467-955-2; Sequence 2, Application US/08467955; Patent No. 5728805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
                                                                                                Query Match 96.2%;
Best Local Similarity 96.2%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 104 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
                          ; MOLECULE TYPE: protein US-08-875-811-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                   96.2%; Score 560; DB 3; Length 355; 96.2%; Pred. No. 6e-60; tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: Modawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, Bighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/875,811

FILING DATE: 19-FEB-1998

CLASSIFICATION NUMBER: US/08/875,811

FILING APPLICATION AA:

APPLICATION NUMBER: WO PCT/US97/02588

FILING DATE: 19-FEB-1997

RADOR APPLICATION NUMBER: WG 60/011,800

FILING DATE: 21-FEB-1996

APPLICATION NUMBER: US 60/010

FELERACCOMMUNICATION: NUMBER: US 60/010

FELERACCOMMUNICATION INPORMATION:

TELEPHONE: (415) 576-0300

INPORMATION FOR SEQ ID NO: 55:

SEQUENCE CHARACTERISTICS:

LENGTH: 366 cmino acids

LENGTH: 366 cmino acids

LENGTH: 366 cmino acids
                                                                                                                                                                                                                                                                        NAME/KEY: Protein
i LOCATION: 1..355
CTHER INFORMATION: /note= "E6FB[Met-(-1)]Serronc"
US-08-875-811-6
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MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 55, Application US/08875811; Patent No. 6045793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 366 amino acids
amino acid
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 96.2
Matches 101; Conservative
                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-875-811-55
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                                                                                                                     1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT
                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TILLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. BOX E
CITY: Short Hills
Score 560; DB 3; Length 366;
Pred. No. 6.2e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                      322 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 366
                                                                                                                                                                                                                                     61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
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1 MSDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVII 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 64, Application US/08875811
Fatent No. 6045793
GENERAL INFORMATION
FAPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
ITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,811
FILING DATE: 19-FEB.1998
CLASSIFICATION NUMBER: WO PCT/US97/02588
RILNG APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB.1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
RILNG DATE: 21-FEB.1996
ATTOMET/AGENT INFORMATION:
ANAMER AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.2%; Score 560; DB 3; 96.2%; Pred. No. 6e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor
                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDERR: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTATION NUMBER: 41,739
REGISTATION NUMBER: 41,739
REGISTATION NUMBER: 915280-244100US
TELEFONMUNICATION INFORMATION:
TELEFONMUNICATION INFORMUNICATION INFORMUNICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORM
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REFERENCE/DOCKET NUMBER: 015280-244100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 355 amino acids
amino acid
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Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-875-811-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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Pred. No. 6e-60;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
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Fatent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Boque, Lluis
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Bighth Floor
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
FILING APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGBNT INFORMATION:
NAME: FATIS, SUSAN K.
REGISTRATION NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
MATTORNEY/AGBNT INFORMATION:
NAME: FATIS, SUSAN K.
REGISTRATION NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 355 amino acids
amino acid
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STATE: California
                         San Francisco
California
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Best Local Similarity
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                                                                                                   COUNTRY:
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US-08-875-811-61
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                                                                           8 MSDWLIFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLI 67
                                            1 MSDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
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Pred. No. 3.8e-60;
2; Mismatches 2; Indels
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                                                                                                                                  61 TSEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 105
                                                                                                                                                                            68 TSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC 112
  2; Indels
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
UNMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor STREET: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFFCATION: 435
CLASSIFFCATION: 435
FILING APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: W0 PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan
REFERENCE/DOCKET NUMBER: 41,739
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         Sequence 59, Application US/08875811
Patent No. 6045793
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TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 59: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 96.2<sup>3</sup>
Matches 101; Conservative
Matches 101; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                               Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak,
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US-08-875-811-59
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Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Modue, Lluis
APPLICANT: Modue, Lluis
APPLICANT: Roque, Recombinant Ribonuclease Proteins
                                                                            APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluis
APPLICANT: Wlodawer, Allaxander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
Sequence 61, Application US/08875811 Patent No. 6045793 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41,739
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INPORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 96.2
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Faris, Susan K. REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                       USA
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RESULT 3

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search,

7, 2004, 21:28:45 ; Search time 12.1796 Seconds (without alignments) 445.066 Million cell updates/sec May Run on:

US-09-961-400-13

582 1 MSDWLTFQKKHLTNTRDVDC.....TFCVTCENQAPVHFVGVGHC 105 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

389414 segs, 51625971 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: /cgr2_6/ptodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:* Issued Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Appl	Appl	Appl	Appl	Appl	Appl	Appl	ilaak	Appl	Appl	Appl	Appl	Appli	Appli	ilady	Appl	Appli	Appli	Appli	Appli	'ppli	Appli	Appli	Appl	Appl	, Appl	Appl
	ជ្ជ	32,	59.	61,	49.	57,	64,	55,	•		41,			1, ,	1, 7	1, 7	13,		1, 7	1, 7	1, 7	1, 7	1, 7	1, 7	28,	30,	63,	45,
	Description	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
n		1-3	11-59	1	11-49	811-57	11-64	11-55	55-2	811-39	11-41	811-51	11-26	971-1	19-1	955-1	48-13	811-1	58-1	72-1	748-1	88-1	29-1		11-28	'n	9-	811-45
SUMMAKIES	ID	1 1	US-08-875-81	US-08-875-8	-875-	-875-	US-08-875-8	US-08-875-8	US-08-467-9	-08-875-	US-08-875-8	US-08-875-8	-875-	US-08-283-9	17-921-	US-08-467-9	-891-	US-08-875-8	US-09-394-2	US-09-071-672-	US-09-687-7	US-08-626-2	-09	-09	0	-08	-08-875-	US-08-875-8
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οķο	Query Match 1	96.2	96.2	96.2	96.2	96.2	96.2	96.2	95.5	95.5	95.5	95.5	95.4	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7	94.7
	Score	260	260	260	260	260	260	260	556	556	556	556	555	551	551	551	551	551	551	551	551	551	551	551	551	551	551	551
	Result No.		2	m	4	ហ	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22		24	25	26	27

53, Appl	43, Appl	4, Appl	, Appl	, Appl	, Appl	, Appl	O, App	7, App	22, App	, Appl	, Appli	, Appli	2, Appl	, Appl.	Appl:	, Appl:	, Appli	
Sequence 5	Sequence 4	Sequence	Sequence 2			Sequence 2	Sequence 3	Sequence 3	Sequence 1	Sequence 8	Sequence 4	Sequence 2	Sequence 1					
US-08-875-811-53	US-08-875-811-43	US-08-875-811-24	US-08-626-288-2	US-09-095-429-2	US-09-394-268-2	US-09-687-748-2	US-08-875-811-20	US-08-875-811-47	US-08-875-811-22	US-08-875-811-2	US-09-071-672-3	US-09-986-119-3	US-08-891-848-12	US-08-875-811-8	US-09-223-118-4	US-09-223-118-2	US-09-223-118-1	
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Sequence 32, Application US/08875811
| Patent No. 6045793 |
| GENERAL INFORMATION: |
| PAPLICANT: Newton, Dianne L. |
| APPLICANT: Boque, Liuis |
| CORRESPONDENCE |
| CORRESPONDENCE |
| ADDRESSEE: Townsend and Townsend and Crew LLP |
| STREET: Two Embarcadero Center, Eighth Floor |
| CITY: San Francisco |
| STATE: California |
| COUNTRY: USA |
| COMPUTER READABLE FORM: |
| MEDIUM TYPE: Floppy disk |
| COMPUTER: IBM PC Compatible |
| OPERATING SYSTEM: PALODENCE |
| OPERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUTWARES PATECHIN RELEASE #1.0, Version SUFWARES PATENTIN RELEASE #1.0, Version APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION ATS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
FILING DATE: 19-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: FAIS, SUSAN K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAN: (415) 576-0200
TELEPRAN: (415) 576-0300
SECURACE CHARACTERISTICS:
CHARACTERISTICS:
TELEPRAN: LIZ AMINO ACIGS
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RESULT 1
US-08-875-811-32
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Length 112;

96.2%; Score 560; DB 3; 96.2%; Pred. No. 1.3e-60;

Query Match Best Local Similarity

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Fur. J. Biochem. 219:641-646(1994).

Eur. J. Biochem. 219:641-646(1994).

-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphate intermediates.

-!- Subcellular Location Secreted.

-!- SUBCELLULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

PIR; 54111; 54111.

RSP; P00656, 1LSO.

InterPro; IPRO01427; RNaseA.

PRODOR; P000504; rnaseA; 1.

RRINTS; PR00794; RIBONUCLEASE.

RRINTS; PR00794; RIBONUCLEASE.

RROSIT; SM00092; RNASE PC: 1.

RRAST; SM00092; RNASE PO: 1.

RRAST; MOUGOS: RNASE PO: 1.

RRAST; MOUGOS: RNASE PO: 1.

RRAST; MOUGOS: RNASE PANCREATIC; 1.

RRAST; MOUGOS: RNASE PANCREATIC; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

PROSITE; PS00127; RNASE PO: 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
Iguana iguana (Common iguana).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
                                                                                                            [1] SEQUENCE.
TISSUB-PADOTEAS;
MEDLINE=94139745; PubMed=8307028;
Zhao W. Beintema J.J., Hofsteenge J.;
"The amino acid sequence of ignana (Ignana) pancreatic ribonuclease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.9%; Score 126.5; DB 1; Length 119; 29.8%; Pred. No. 8.4e-07; tive 16; Mismatches 51; Indels 13;
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Best Local S:
Matches 34
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ACT SITE
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Search completed: May 11, 2004, 14:35:05 Job time: 11.0452 secs

4

Indels 13; Gaps

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151 AA.

STANDARD;

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RNBR_AXIPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --STTRFQLNTCTRTSITPRP-CPYSSRTEINYICVKCE-NQY-PVHFA 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 31-114 FROM N.A.
MEDLINE-93367815; PubMed=836016;
Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P., Carsana A., Palmieri M., Furia A.;
"Sequences related to the ox pancreatic ribonuclease coding region in the genomic DNA of mammalian species.";
J. Mol. Bvol. 37:29-35(1993).
-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                              Giraffa camelopardalis (Giraffe).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT SITE (2012). MICLEASE;                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96139017, PubMed=8587129;
Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
Vento M.T., Furia A.;
"Molecular evolution of genes encoding ribonucleases in ruminant

    -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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30.6%; Pred. No. 7.8e-07;
   update)
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   Last annotation u
C 3.1.27.-) (BRB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
16-OCT-2001 (Rel. 40, Last annotat
Ribonuclease, brain (EC 3.1.27.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Evol. 41:850-858(1995).
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PRINTS, PR00794, RIBONUCLEASE.
ProDom, PD000535, RNaseA, 1.
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                                                                                                                                                                    Mammalia; Eutheria;
Giraffidae; Giraffa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 NITCKNGQPNCYQSNSTMNITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                             Axis porcinus (Hog deer).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Buthoria, Cetartiodactyla, Ruminantia, Pecora, Cervoidea,
Cervidae, Cervinae, Axis.
                                                                                                                                                                                                                                                                                                                                                                                           Secretory ribonuclease genes and pseudogenes in true ruminants."; sene 212:259-268(1998).
                                                                                                                                                                                                                                                                                                         MEDLINE-98278842; PubMed-9611269;
Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
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84 BY SIMILARITY.

95 BY SIMILARITY.

110 BY SIMILARITY.

72 BY SIMILARITY.

62 N-LINKED (GLCNAC. . . ) (BY & CO-LINKED (BY SIMILARITY).

129 O-LINKED (BY SIMILARITY).

131 O-LINKED (BY SIMILARITY).

131 BS5F3757FFC5B233 CRC64;
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N-LINKED (GLCNAC. . .) (B)
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Pred. No. 8.4e-07;
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Last annotation update)
                15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease, brain (EC 3.1.27.-) (BRB).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
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15-DEC-1998 (Rel. 37, Created)
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30.6%;
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01-FEB-1994
28-FEB-2003
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P80<u>2</u>87;
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RNBR_AXIPR RESULT 14

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59 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCENQ--YPVHF 104
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InterPro; IPR001427; RNaseA.
Pfam; PR00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SNART; SM00092; RNASE Pc; 1.
PROSITE; PS00127; RNASE PANCERATIC; 1.
Hydrolase; Nuclease; Endonuclease, Angiogenesis; Protein synthesis inhibitor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
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Pred. No. 6.8e-07;
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                                                                                    123 AA
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                                                                                                                                                 Angiogenin-2 (EC 3.1.27.-)
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                                                                                     STANDARD;
                                                                                                                                                                                                                                                               TISSUE=Milk, and Serum;
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113
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01-NOV-1997
28-FEB-2003
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ACT_SITE
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                                                                                        6 AKFRRQHMDSGSSSGNPNYCNQMMKRR-RMTHGRCKPVNTFVHESLDNVKAVCS---QK 61
                                                                        7 FOOKHI-----INTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGV-INMN 59
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                                                 Gaps
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Capreolus capreolus (Roe deer).
Capreolus capreolus (Roe deer).
Bukaaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Cervidae; Odocoileinae; Capreolus.
                                                                                                                          104
                                                                                                                                                 67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIVACEGNPPVPVHF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                  "Secretory ribonuclease genes and pseudogenes in true ruminants.";
                                                                                                                          60 VLSTTRFQLNT------CTRTSITPRP-CPYSSRIETNYICVKCENQ--YPVHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                              17;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 212:259-268(1998).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                       Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 151;
                                                 Indels
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W; 392DDE6302F006A6 CRC64;
0AC28CDE14111845 CRC64;
             21.9%; Score 132.5; DB 1;
31.6%; Pred. No. 2e-07;
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29.4%; Pred. No. 6.6e-07;
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PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98278842; PubMed=9611269;
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Pfam; PF000794; rnaseA, 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA, 1.
13804 MW;
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129
 124 AA;
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les 36; Conserv
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nes 35; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **MEDLINE-97409980; PubMed=9266695; Strydom D.J., Bond M.D., Vallee B.L.; **A magiogenic protein from bovine serum and milk -- purification an primary structure of angiogenin-2."; Eur. J. Biochem. 247:535-544(1997).

-- FUNCTION: Binds tightly to placental ribonuclease inhibitor and has very low ribonuclease activity. Has potent angiogenic activity. Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs.
-- TISSUE SPECIFICITY: Serum and milk.
-- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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Conservative
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                                                                                 59 NVL----
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                                                                                                                                             106 G 106
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 38;
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                                                                                                                                                      Sasso M.P., Carsana A., Confalone B., Cosi C., Sorrentino S.,
Viola M., Palmieri M., Russo B., Furia A.;
"Molecular cloning of the gene encoding the bovine brain ribonuclease
and its expression in different regions of the brain.";
Nucleic Acids Res. 19:6469-6474(1991).
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                      Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y., Ohgi K., Irie M.; "Primary structure of a ribonuclease from bovine brain.";
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96139017; PubMed=8587129; Octalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M., Vento M.T., Furia A.; Molecular evolution of genes encoding ribonucleases in ruminant
                                                                                                                                                                                                                                                                                                                                                                                                                                           or. Mol. Bvol. 41:850-858(1995).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 133.5; DB 1; Length 167; Pred. No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T -> S (IN REF. 2).
681CAAC3CC2FC459 CRC64;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. ..).
/FTIG-CAR_000005.
                                                                                                                                                                                                                                              SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES
16-OCT-2001 (Rel. 40, Last annotation update)
Ribonuclease, brain precursor (EC 3.1.27.-) (BRB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIBONUCLEASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-LINKED
                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=92093604; Pubmed=1754384;
                                                                                                                                                                                                                                                                         MEDLINE=89214015; PubMed=3243767;
                                                                                                                                                                                                                                                                                                                                   J. Biochem. 104:939-945(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18450 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.0%;
31.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S81744; AAB36138.1; -.
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HSSP; P00656; 2RNS.
GlycoSuiteDB; P39873; -.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 27-167 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00074; rnaseA; 1
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167
38
67
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159
155
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110
121
                                                                                   Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155
159
155
167 AA;
                                           taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                NCBI_TaxID=9913;
                                                                                                                                                                                                                                                             IISSUE=Brain;
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7;
                                                                                          --STIRFQLNICIRISIIPRP-CPYSSRIEINYICVKCE-NQY-PVHFA 105
                                                                                                                       88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPNCAYKTSQKQKYITVACEGNPYVPVHFD 147
                              5 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINM 58
                                                           32 AKFRROHMDSGSSSSSNPNYCNOMMKRR-RMTHGRCKPVNTFVHESLDDVKAVCS---QK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wherenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J., "Affihity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence."; FEBS Lett. 31:181-185(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.

    J. Biol. Chem. 245:654-661 (1970).
    -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside phosphate and 3'-phosphooligonucleotides ending in C-P or with 2', 3'-cyclic phosphate intermediates.
    -!- SUBCELLULAR LOCATION: Secreted.

 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jackson R.L., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. II.
amino acid sequence of the reduced S-aminoethylated protein.";
J. Biol. Chem. 245:637-653(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=70104198; PubMed=4904878;
Phelan J.J., Hirs C.H.W.;
"The primary structure of porcine pancreatic ribonuclease. 3.
disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- TISSUE SPECIFICITY: Pancreas.
                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
 43; Indels
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N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
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                                                                                                                                                                                                                                                                 124 AA
 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodom; PD000535; RNaseA; 1.
SWART; SW00092; RNAse Pc; 1.
PROSITE; PS00127; RNASE PanCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=70104197; PubMed=5460946;
                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00794; RIBONUCLEASE.
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InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                 STANDARD;
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119
120
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ACT_SITE
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CARBOHYD
CARBOHYD
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human and mouse cDNA sequences.";
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ID RNBR BOVIN
AC P39873;
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                                                                                                                                                                                                                                                                                                                 HSSP;
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                                                                                                                                                                                                                                                                              64 LCKNGRINCYESNSTMHITDCRQTGSSKYPNCAYKTSQKEKHIIVACEGNPYVPVHF 120
                                                                                                                                                                                                                                                                  61 L-----STTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 104
                                                                                                                                                                                                                           7 FQQKHII------NTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                              8 FOROHMDSGNSPGNNPNYCNOMMRR-KMTOGRCKPVNTFVHESLEDVKAVCS---OKNV
                                                                                                                                                                                                         23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                 01-WAY-1991 (Rel. 18, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Anglogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
                                                                                                                                                                                      DB 1; Length 124;
                                                                                                                                                         .) (30%).
                                                                                   95 BY SIMILARITY.
96 BY SIMILARITY.
110 BY SIMILARITY.
72 BY SIMILARITY.
12 BY SIMILARITY.
14 BY SIMILARITY.
119 BY SIMILARITY.
110 BY SIMILARITY.
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bond M.D., Vallee B.L.; "Isolation and sequencing of mouse angiogenin DNA."; Biochem. Biophys. Res. Commun. 171:988-995(1990).
                                                                                                                                                                                              9.4e-08;
ches 39;
                                                                             Glycoprotein.
                                                                                                                                                                                  Query Match

22.44;

Best Local Similarity 33.34; Pred. No. 9.4e.

Matches 39; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                     145 AA
        HSSP; P00656; ISRN.
InterPro; IPR001427; RNaseA.
InterPro; IPR001427; RNaseA.
Ffam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNASE PANTEATIC; 1.
PROSITE; PS00127; RNASE PANTEATIC; 1.
Hydrolase; Nuclease; Endonuclease; Glycop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91025023; PubMed=2222458;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       (Mouse)
                                                                                                                                                                   124 AA;
PIR; A00818; NRWHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                         58
65
12
41
119
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P21570;
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                                                                                                DISULFID
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                                                                                                                                                SITE
                                                                                                                                                                    SEQUENCE
                                                                                                         DISULFID
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                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; FROOT, RIBORNCLEASE.
PRODOM; PROOFS; RNaseA; 1.
PRODOM; PROOFS; RNASE Pc; 1.
PROSITE; PSOOL27; RNASE Pc; 1.
Hydrolase; Nuclease; Endonuclease; Anglogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                        MEDLINE=93192291; PubMed=8448182;
Bond M.D., Strydom D.J., Vallee B.L.;
"Characterization and sequencing of rabbit, pig and mouse
angiogenins: discernment of functionally important residues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06944260BB764938 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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(Rel. 31, Last sequence update)
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123 FRHVVIACENGLPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:88022; Ang.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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                                   PARTIAL SEQUENCE.
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64
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                                                         TISSUE=Serum;
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01-FEB-1995
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EMBL; U22519; AAA91367.1; -. HSSP; P03950; 1A4Y.
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25
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137
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P00673;
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ACT_SITE
DISULFID
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                                                                                                                                                                                                                                   CHAIN
MOD_RES
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the burpopen Bioinformatics Institute. There are or erstrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                  and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CKRVNTFIISSATTVKAIC-----TGVINMNVLSTTRFQLNTCTRTSITPR-PCPYSSR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=129; TISSUB=Liver; MEDLINE=96079109; PubMed=8530072; Brown W.E., Noblie V., Subramanian V., Shapiro R.; Brown W.E., noblie V., Subramanian V., Shapiro R.; The mouse anglogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes."; Genomics 29:200-206(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
                            -:- FUNCTION: Angiogenin induces vascularization of normal and malignant tissues. Abolishes protein synthesis by specifically hydrolyzing cellular tRNAs (By similarity)
-:- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                   ProDom; FULUVOSJ, SMASE PC; 1.
PROSITE; PSOUG2; RNASE PC; 1.
PROSITE; PSOUG2; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Angiogenesis;
Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                 25.5%; Score 154.5; DB 1; Length 145;
developmentally regulated genes when expressed in NIH 3T3
                                                                                                                                                                                                                                                                                             ANGIOGENIN-3.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Indels
                                                                                                                                                                                                                                                                                                                                                                                             DE9D3BC92F1D682C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Anglogenin-related protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 AA.
                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                   Biol. 17:1503-1512(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 TETNYICVKCENOYPVHF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 KDFRYIVIACEDGWPVHF 138
                                                                                                                                                                                       MGD; MGI:1201793; Angl.
InterPro: IFRO01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                             16696 MW;
                                                                                                                                                                   EMBL; U72672; AAC05794.1; -. HSSP; P10152; 1AGI.
                                                                                                                                                                                                                                                                                                                                                                                                                            43.68;
                                                                                                                                                                                                                                  PD000535; RNaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                              37
64
137
104
115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                             37
64
137
50
13
63
145 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
           fibroblasts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANGR_MOUSE
Q64438;
                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                            DISÜLFID
DISULFID
                                                                                                                                                                                                                                                                                                                                SITE
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                 ProDom;
                                                                                                                                                                                                                                                                                                           MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CKDVNTFIHDTKNNIKALCGKKGSPYGRNLRISKSRFQVTTCTHKGRSPRPPCRYRASKG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 CKRVNTFIISSATTVKAIC---TGVINMNV-LSTTRFQLNTCTRISITPR-PCPYSSRIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribonuclease.";
Biochem G. 1.57:317-323(1976).
Biochem G. 1.57:317-323(1976).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
with 2', 3'-cyolic phosphate intermediates.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Pancreas.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emmens M., Welling G.W., Beintema J.J.;
"The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Balaenoptera acutorostrata (Minke whale) (Lesser rorqual).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Cetacea, Mysticeti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.7%; Score 149.5; DB 1; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANGIOGENIN-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29A6EB814429C4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:104984; Angrp.
InterPro; IPR001427; RNSSEA.
PEMM: PR00074; TNBSEA. 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNASSEA; 1.
SWART; SW00092; RNASSE Po; 1.
PROSITE; PS00127; RNASE Po; 1.
PROSITE; PS00127; RNASE Pouclease;
Signal, Hydrolase; Nuclease;
Pyrrolidone carboxylic acid. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AA.
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SIMILARITY.
SIMILARITY.
SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 FRYILIGCENGWPVHF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 TNYICVKCENQYPVHF 104
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-!- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fu X., Kamps M.P.; "E2a-Pbx1 induces aberrant expression of tissue-specific and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.0%; Score 272.5; DB 1;
49.1%; Pred. No. 1.4e-22;
iive 15; Mismatches 32;
                                                                                                                                      Hydrolase; Nuclease; Endonuclease; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 AA
                                                                                                    ProDom, PD000535; RNaseA; 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BALB/c;
MEDLINE=97184476; PubMed=9032278;
                                                                                                                                                                                                                                                                                                                                                                                                                                          11845 MW;
                                                                 PDB; 10NC; 31-JAN-94.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
                                                                                                                                                     acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                  Pyrrolidone carboxylic
                                                                                                                                                                                             50
70
75
75
91
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Mus musculus (Mouse)
             against several
                                                                                                                                                                                                                                                                                                                                                                                                                                          104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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31
31
19
30
48
87
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P97802;
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DISÜLFID
                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                     SITE
                                                                                                                                                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                                                        3 NWATFQOKHIINTPII-CNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                        2 NWAKFKEKHIRSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE
                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comparative molecular modeling and crystallization of P-30 protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ап

    CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphate intermediates.
    with 2', 3'-cyclic phosphate intermediates.
    SUBCELLULAR LOCATION: Secreted.
    SIMILARITY: Belongs to the pancreatic ribonuclease family.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Embryo;
MEDLINE=91093131; PubMed=1985896;
Ardelt W., Mikulski S.M., Shogen K.;
"Amino acid sequence of an anti-tumor protein from Rana pipiens cocytes and early embryos. Homology to pancreatic ribonucleases.";
J. Biol. Chem. 266:245-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-FRB-1994 (Rel. 28, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
P-30 protein (EC 3.1.27.-) (Onconase).
P-30 protein (EC 3.1.27.-) (Aughliare (Northern leopard frog).
Eukaryota; Metazoa; Ghordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDILINE=94166079; PubMed=8120892;
Mosimann S.C., Ardelt W., James M.N.G.;
Refined 1.7 A X-ray crystallographic structure of P-30 protein,
amphibian ribonuclease with anti-tumor activity.";
J. Mol. 236:1141-1153(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93066156; PubMed=1438177;
Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
                                                                                                                                                                                                                                                                                                                                                                      61 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                     62 LSTISFKLNICIRDSITPRPCPYHPSPDNNKICVKCEKQLPVHFVGIGKC 111
                                                                                                                                                 Length 111;
                                                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                                                                        D64BA72456C10788 CRC64;
                                                                                                                                                                                                                                                                            Score 369; DB 1;
Pred. No. 6.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 AA
                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
                                                                                                                                        PANCREATIC, 1.
                                                                                                                                                                                                                                                       12461 MW;
  106:729-735 (1989)
                                                                                        Diterpro; IPR001477; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCT
                                                                                                                                                                                                                                                                            65.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins 14:392-400(1992).
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3D-STRUCTURE MODELING.
                                                                     PIR; JX0085; JX0085.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Loca 72; Conserve
                                                                                                                                                                                                                                                        AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        James M.N.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                   molecular weight ribosomal RNA.
-!- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
ainst several tumor cell lines in vitro, as well as antitumor vivo. It exhibits a ribonuclease-like activity against high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anglogenin-3 precursor (EC 3.1.27.-) (Anglogenin-related protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin aggliniates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NWATFQOKHINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STTRFQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STTRFQLNTCTRTSITPRDCPYSSRTETNYICVKCENOYPVHFAGIGRCP 133
                                                                            -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.8%; Score 586.5; DB 1; Length 133; 99.1%; Pred. No. 3.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                       RIBONUCLEASE, OOCYTES.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14762 MW; A7D62594F7D16F0C CRC64;
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                                                                                                                                                                                                                                 EMBL; AF039104; AAD10702.1; -.
                                                                                                                                                                                                                                           PIR; A27121; A27121.
PDB; 1BC4; 28-OCT-98.
PDB; 1MO7; 21-JAN-09.
InterPro; IPR01427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; P0000535; RNaseA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Matches 109;
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P18839;
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Last sequence update)
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(Rel. 16, Created) (Rel. 28, Last seq. (Rel. 42, Last anno

01-NOV-1990 01-FEB-1994

10-OCT-2003

111 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                      -i- FUNCTION: The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin preferentially agglutinate a large variety of tumor cells, but it does not agglutinate non-transformed cells and erythrocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NWAKFQEKHIPNTSNINCNTIMDKSIYIVGGCKERNTFIISSATTVKAICSGASTNRNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                     TISSUE=Egg;
MEDLINE=91035319; PubMed=2229005;
Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
Takayanagi Y., Titani K.;
                                                                                                                                                                 Amino acid sequence of a lectin from Japanese frog (Rana japonica)
Sialic acid-binding lectin (EC 3.1.27.-).
Rana japonica (Japanese reddish Erog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
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Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
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Okazaki T., Ohgi K., Irie M.;
                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
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                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001427; RNaseA.
Pfam; PF00074; TnaseA; 1.
Smarr; SM000515; RNaseA; 1.
SMART; SM00092; RNASE Pc; 1.
SPROSTIES; PS00127; RNASE PANCREATIC; 1.
Hydrolase; Nuclease; Banchouclease; Sialic acid; Lectin; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12326 MW; FDEBDDF3834ED679 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.3%; Score 450; DB 1; 78.2%; Pred. No. 1.2e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-787-1990 (Rel. 14, Created)
01-FBR-1994 (Rel. 28, Last sequence update)
28-FBR-2003 (Rel. 41, Last annotation update)
18-FBR-2003 (Rel. 41, Last annotation update)
Rana catesbeiana (Bull frog).
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SIMILARITY.
SIMILARITY.
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BY
                                                                                         SEQUENCE, AND DISULFIDE BONDS.
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HSSP; P11916; 1BC4.
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                                                           NCBI TaxID=8402;
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us-09-961-400-26.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:24:28; Search time 10.0452 Seconds (without alignments) 575.375 Million cell updates/sec

Title: US-09-961-400-26
Perfect score: 606
Sequence: 1 MSNWATFQQKHIINTPIICN......ICVKCENQYPVHFAGIGRCP 1111
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Gapop 10.0 , Gapext 0.5 ed: 141681 segs, 52070155 residues

Searched:

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100*
Maximum Match 100*
Listing first 45 summaries

Listing lirst 45 summar

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P11916 rana catesb	P18839 rana japoni	rana	rana	mus m		P00673 balaenopter		P39873 bos taurus		P79351 capreolus c		-							P00668 antilocapra	P00686 macropus ru	P00676 myocastor c	Q8wn67 pongo pygma	P00683 mus musculu	Q8wn61 aotus trivi				-	P00670 camelus dro	proe		Q8wn63 macaca mula
SUMMAKIES	ID De	RNPO RANCA P1		RNPL RANCA P1	RN30 RANPI	ANG3 MOUSE PS	ANGR MOUSE Q6	RNP BALAC PO	ANGI MOUSE P2	RNBR_BOVIN P3	pId	RNBR CAPCA	ANG2_BOVIN P8		~	Guig	ANGI CERAE QE	ANGI_MIOTA Q8		SHEEP			MYOCO	→		AOTTR	PIG	CAVPO	E	HORSE	RNP_CAMDR P(ANGI_MACMU QE
	° Query Match Length DB	133 1			104 1							151 1					146 1		146 1	143 1	124 1	122 1	128 1		149 1		123 1		146 1			m	119 1	146 1
o\e	Query Match	96	74	9	45.0	25	24	7		22.0	21.9	21.2	21.0	21.0	21.0	20.9	20.9	20.9	20.6	20.4	20.2		19.9	9.	19.9	19.	19.	13	19.	19.	_	19.2	19.1	19.1
	Score	586.5	450	369	272.5	154.5	149.5	135.5	135.5	133.5				10			126.5				122.5	122	120.5	120.5	120.5	120	119.5	118.5	118	117.5	116.5	116.5	115.5	
	Result No.		2	3	4	5	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29	30	31	32	33

P10152 bos taurus P00666 rangifer ta	P31347 oryctolagus Q8wn64 papio hamad	203950 nomo saplen Q8wme8 pan troglod	P00664 capreolus c P00662 giraffa cam	09jjhl mus musculu P24717 cricetulus	OSS004 rattus norv	Q9wtts acomys can:
ANGI BOVIN RNP RANTA	ANGI_RABIT ANGI_PAPHA	ANGI HUMAN ANGI PANTR	RNP_CAPCA RNP_GIRCA	RNS4 MOUSE RNP CRILO	RNS4 RAT	RNP_ACOCA
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148	125	147	124	148	147	149
18.8	18.7	18.6 18.6	18.6 18.6	18.6	18.4	18.4
113.5	113.5	113	112.5	112.5	111.5	111.5
ሌ ሬ 4 ቢ	34	8 6 9 6	4 4 1	4.4 2.43	44	45

ALIGNMENTS

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MEDLINE=98437383; PubMed=9761686; Chang C.F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.; Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.; "The solution structure of a cytotoxic ribonuclease from the occytes Gana catesbeana (bullfrog)."; J. Rol. Biol. 283:231-244[1998].
-I. FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
                                 P119T6; Q9PWR7;
01-0CT-1989 (Rel. 12, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Egg;
MEDLINE=87299649; PubMed=3304421;
Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
Takayanagi G., Hakomori S.,
"Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";
                                                                                                                                                                                                                                                                                    MEDLINE=98165825; PubMed=9497370;

Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;

"The Rana catesbelana rcr gene encoding a cytotoxic ribonuclease.

Tissue distribution, cloning, purification, cytotoxicity, and active
residues for RNase activity.";

J. Biol. Chem. 273:6395-6401(1998).
                                                                                                                                                          Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A pyrimidine-quanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
Nucleic Acids Res. 20:1371-1377(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IISSUE=Egg;
MEDLINE=93192604; PubMed=8448385;
Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
Takayanagi Y., Hakomori S., Titani K.;
"Ribonuclease activity of stalic acid-binding lectin from Rana
                    133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION, AND SEQUENCE OF 81-101.
MEDLINE=92220613; PubMed=1373237;
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 26:2189-2194(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycobiology 3:37-45(1993).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 23-133.
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 23-133.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catesbeiana eggs."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
                                                                                                                                                                                                                  NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                           TISSUE=Liver;
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                      RNPO RANCA
RNPO_RANCA
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1 SNWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NWN 58
                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Gln1Ser substitution
; OTHER INFORMATION: (recombinant RaPIR1 Q1S)
US-09-948-391A-11
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 49.5%; Pred. No. 4.5e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9;
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9; Gaps

Search completed: May 11, 2004, 14:39:23 Job time : 38.8281 secs

69 TTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

a

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2 NWATFQQKHIIKTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNVLS 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: cateabelana ribonuclease with Met22Leu and OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1 OTHER INFORMATION: Met22Leu Met57Leu)
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APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Serepresented by The Secretary of the
APPLICANT: Serepresented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: WS 60/079,751
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: WS 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
                                                                                                                                                                                                                                                                                                                                               FILE REFRENCE: 015280-34310US
CURRENT APPLICATION: Recombinant Anti-Tumor RNase
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR PRILING DATE: 1999-03-26
PRIOR PRILING DATE: 1999-03-26
PRIOR FILING DATE: 1900-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
                                                                                                                                                                                                                                               Newton, Dianne L.
The United States of America
as represented by The Secretary of the
Department of Health and Human Services
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97.2%; Pred. No. 1.2e-58;
iive 2; Mismatches 1
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                                                                                                                                  Application US/09948391A
                                                                                                                                     Sequence 19, Application US/099, Publication No. US20030027311A1; GENERAL INFORMATION: APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 106; Conservative
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                                                                                  RESULT 14
US-09-948-391A-19
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LENGTH: 104
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PUBLICATION NO. US20030124131A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT:

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT:

TITLE OF INVENTION: CELLS

FILE REFERENCE: 018733/1059

CURRENT FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 2:

LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbelana ribonuclease with (His)6 tag, Met at
OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
OTHER INFORMATION: (recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.3%; Score 591; DB 10; Length 117; 98.2%; Pred. No. 2.7e-59; ive 2; Mismatches 0; Indels (
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Pred. No. 2.7e-59;
2; Mismatches 0;
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
                   FILE OF TRYNATION, NO.2200.
FILE REFERENCE: 015280-34311005
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 22
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98.2%;
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Matches 107; Conservative
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Best Local Similarity
Matches 107; Conserv
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US-09-961-400-22
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                               62 TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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98.3%; Score 591; DB 10; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.5e-59;
Matches 108; Conservative 0; Mismatches 1; Indels (
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APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPRENCE: 015280-3431100S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT RILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SOFTWARR: SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                 APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR PILIOR DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR PLILNG DATE: 2000-08-17
NUMBER OF SEC ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                 Sequence 17, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             APPLICANT: Rybak, Susanna M.
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TAPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REPRENCE: 018733/1059
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ 1D NOS: 43
SOFTWARE: PATCHIN UNS: 43
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                                                                                                                                                                                                                                                                                                          Gaps
                                                                          OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1, OCTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant OTHER INFORMATION: Met.-1, RacORI Met22Leu Met57Leu)
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The United States of America
as represented by The Secretary of the
Department of Health and Human Services
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                                                                                                                                                                                                                                              98.3%; Score 591; DB 10;
98.2%; Pred. No. 2.5e-59;
iive 2; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-961-400-21
, Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Newton, Dianne L
APPLICANT: The United States
APPLICANT: as represented by
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ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                           Query Match 98.3
Best Local Similarity 98.2
Matches 107; Conservative
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Best Local Similarity
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SEQ ID NO 19
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| Sequence 15. Application No. US20030124131A1
| GENERAL INFORMATION:
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: RYBAK, SUSANNA M. |
| APPLICANT: ROLDENBERG, DAVID M. |
| APPLICANT: NEWTON, DIANNE L. |
| TITLE OF INVENTION: CELLS |
| FILE REFERENCE: 0.1873/1059 |
| CURRENT APPLICATION NUMBER: US/09/961,400 |
| CURRENT FILING DATE: 2000-08-17 |
| PRIOR PLICATION NUMBER: 06/622,613 |
| PRIOR PLICATION NUMBER: 06/622,613 |
| PRIOR FILING DATE: 1999-03-26 |
| PRIOR FILING DATE: 1999-03-26 |
| PRIOR FILING DATE: 1999-03-26 |
| NUMBER OF SEQ ID NOS: 43 |
| SOFTWARE: PARCHIN VET. 2.1 |
| SERVING APPLICATION NUMBER: 06/079,751 |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic OTHER INFORMATION: gene modified to use E. coli preferred codons
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Best Local Similarity 100.0%; Pred. No. 5.2e-60;
Matches 109; Conservative 0; Mismatches 0;
                           PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR PLILING DATE: 2000-08-17
NUMBER: OF SEQ ID NOS: 43
SEQ ID NO 15
PRIOR APPLICATION NUMBER: US 60/079,751
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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; ORGANISM: Rana catesbeiana
US-09-961-400-15
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US-09-961-400-15
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RESULT 7 US-09-961-400-17

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APPLICANT: SYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REPERENCE: 018733/1059
CURRENT APPLICATION NUMBER: 09/622,613
FRIOR FILING DATE: 2001-09-25
FRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 09/622,613
FRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PRILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PARENTIN UVER: 2.1
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GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT:
TITLE OF INVENTION: CELLS
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Pred. No. 5.3e-60;
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CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
Sequence 17, Application US/09961400
                   Publication No. US20030124131A1
GENERAL INFORMATION:
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ORGANISM: Rana catesbeiana
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SOFTWARE: PatentIn Ver. 2.1
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Matches 109; Conservative
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US-09-961-400-19
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US-09-948-391A-15
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US-09-961-400-26
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                                                                                                                                                                                                                                                       PUDLICATION NO. US20030124131A1

GENERAL INPORMATION:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: GOLDENBERG, DAVID M.

APPLICANT: GOLDENBERG, DAVID M.

TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

FILE REPERANCE: 018733/1059

CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT PILING DATE: 2001-09-25

PRIOR PELING DATE: 2000-08-17

PRIOR PELING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATENTING UNER: 05/079,751

PRIOR FILING DATE: 1998-03-26

NUMBER OF SEQ ID NOS: 43

SEQ ID NO 24

LENGTH: 110
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SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 60
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                                                                                                 SITRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Bepartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015.280-3431100S
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
                                                                                                                                                                                                                            Sequence 24, Application US/09961400 Publication No. US20030124131A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 110; Conserv
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US-09-948-391A-26
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LENGTH: 111
TYPE: PRT
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TAPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONUTGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REPERENCE: 10473714059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: 09/6241
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 43
SOPTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                            ASSIWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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                                                                                                                                                                                                                                   Gaps
OTHER INFORMATION: Description of Artificial Sequence:Rana OTHER INFORMATION: catesbelana ribonuclease with Met at position: OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 Q1S) US-09-948-391A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 STTREQLATCTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                61 STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
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                                                                                                                                                                  Length 111;
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APPLICANT: Newton, Dianne L.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015260-343110US
CURRENT PELLING DATE: 2002-05-10
                                                                                                                                                               100.0%; Score 601; DB 10;
100.0%; Pred. No. 1.8e-60;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 26, Application US/09961400 Publication No. US20030124131A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rana catesbeiana
                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 110; Conservative
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May 11, 2004, 14:34:38; Search time 37.8281 Seconds (without alignments) 807.135 Million cell updates/sec
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1 SNWATFQQKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110
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1. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*

1. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.ppp:*

2. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*

2. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.ppp:*

2. (cgn2_6/ptodata/2/pubpaa/DEUGOMB.ppp:*

3. (cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.ppp:*

3. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*

3. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.ppp:*

4. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.ppp:*

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5. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.ppp:*

6. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.ppp:*

7. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.ppp:*

7. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.ppp:*

8. (cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.ppp:*

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8. (cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.ppp:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1140673 segs, 277566755 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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length: 2000000000
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                   Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 15, Sequence 15, Sequence 19, Sequence Sequence Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-948-391A-24 US-09-961-400-24 US-09-961-400-26 US-09-961-400-26 US-09-948-391A-15 US-09-961-400-17 US-09-961-400-17 US-09-961-400-17 US-09-961-400-17 US-09-961-400-17 US-09-961-400-21 US-09-961-400-22 US-09-948-391A-22 US-09-948-391A-22 US-09-948-391A-22 US-09-948-391A-22 US-09-948-391A-22 US-09-948-391A-22 US-09-948-391A-19 US-09-948-391A-19 Π Match Length DB 601 601 601 601 601 597 591 591 591 591 591 591 591 Score Result

113	Sequence 13, Appl Sequence 2, Appli	9	ý,	28	78	ď	Sequence 9, Appli	Ή,	, e	Sequence 2, Appli	4,	Sequence 4, Appli	œ	Sequence 53, Appl	œ	σ	'n	m	2, 7	103,	89,	Sequence 139, App	Sequence 141, App	Sequence 52, Appl	Sequence 254, App	Sequence 254, App	Sequence 8, Appli
-961 -948	US-09-961-400-13 US-09-961-400-2	US-09-948-391A-6	US-09-961-400-6	US-09-948-391A-28	US-09-961-400-28	US-09-948-391A-2	US-09-961-400-9	US-09-986-119-1	US-09-918-887-1	US-10-153-882-2	US-09-948-391A-4	US-09-961-400-4	US-09-961-400-8	US-10-461-713-53	US-09-948-391A-8	US-09-948-391A-9	US-09-986-119-3	US-09-918-887-3	US-10-016-447-2	US-10-037-417-103	US-10-016-248-89	US-10-074-978A-139	US-10-074-978A-141	1-713-5	US-09-731-872-254	6-997	US-09-981-286A-8
101	100	10	10	10	10	10	10	σ	10	14	10	10	10	12	10	10	σ	10	13	12	12	15	15	17	6	10	σ
104	104	105	105	127	127	104	111	104	104	105	104	104	105	104	105	111	83	83	169	124	119	119	99	124	147	147	124
46.7	46.0	46.0	46.0	46.0	46.0	45.8	45.5	45.3	45.3	45.3	45.0	45.0	45.0	44.0	43.5	43.5	34.3	34.3	26.3	22.5	21.0	21.0	20.1	19.6	19.5	19.5	19,1
280.5	276.5	276.5	276.5	276.5	276.5	275.5	273.5	272.5	272.5	272.5	270.5	270.5	270.5	264.5	261.5	261.5	206	206	158	135.5	126.5	126.5	121	117.5	117	117	114.5
16	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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) OTHER INFORMATION: catesbeiana ribonuclease with GlniSer substitution
) OTHER INFORMATION: (recombinant RaCORI QIS)
US-09-948-391A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                         APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of the Secretary of the September of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 012280-343110US
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: WS 09/622,613
PRIOR APPLICATION NUMBER: WS 09/622,613
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR APPLICATION NUMBER: US 03/622,613
PRIOR PRILING DATE: 2000-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 601; DB 10;
100.0%; Pred. No. 1.8e-60;
iive 0; Mismatches 0;
                        ; Sequence 24, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                             APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States
APPLICANT: as represented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 110; Conservative
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Best Local Similarity
US-09-948-391A-24
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1 SNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL

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1 ODWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 51
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Colobinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bydathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22597544; PubMed=12711394;
Zhang J., Zhang Y.-P.;
"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22597544; PubMed=12711394;
Zhang J., Zhang Y.-P.;
"Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%; Score 129.5; DB 6; Length 146; 34.2%; Pred. No. 4.1e-07; ive 16; Mismatches 40; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 IASKNV-LITSEFYLSDCNV---ISR-PCKYKLKKSINIFCVICENQAPVH 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eating monkey.";
Gene 308:95-101(2003).
Gene 308:95-103(2003).

EMBL, AY221130; AA041317.1; -.

EMBL, AY221130; AA041317.1; -.

EMBL, AY221130; PROU452; F:pancreatic ribonuclease activity; IEA.

R GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

R IncerPro; IPRO0427; RNaseA.

R PFam; PRO0074; RIBONUCLEASE.

R PRINTS; PRO0794; RIBONUCLEASE.

R PROMITS; PRO0192; RNASE PANCREATIC; 1.

R PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               earing monkey.";

Gene 308:95-101(2003).

EMBL, AY221131; AA041338.1;

GO, GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

InterPro; IPR001427; RNaseA.
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PRINTS; PR00794; RIBONUCLEASE.
ProDom: PD000535; RNase, 1.
SMART; SM0092; RNASE PC; 1.
PROSITE; PS00127; RNASE PONCREATIC; 1.
SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;
                                                                                    01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                        146 AA
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                                        PRT;
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                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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NCBI_TaxID=61621;
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                                                                                                                                                                                     Angiogenin.
Q861Y3
DQ861Y3;
DT Q861Y3;
DT 01-JUN-
DT 01-JUN-
DE Angiogen
OC Bukarlyi
OC Pygathr.
OC Py
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                                                       1 ODWLTFOKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI
                               Gaps
                                                                                                                              88 PYGENLRISKSPFQVITCNLRGGSSRPPCRYRATAGFRNIVVACENDLPVH 138
                                                                                                             52 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLKKSTNTFCVTCENQAPVH 97
                              17;
    Length 146;
                              Indels
    DB 6;
22.4%; Score 129.5; DB 6; 34.2%; Pred. No. 4.1e-07; iive 16; Mismatches 40;
                             Conservative
               Local Similarity
                           38;
 Query Match
               Best Loc
Matches
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Search completed: May 7, 2004, 21:46:01 Job time : 31.5753 secs

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EMBL; AF159166; AAD41901.1; -. HSSP; P00656; 1LSQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRL2 protein.
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                                                                                                                                                                                                      Signal.
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Q9W738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 QDWPTFQQKHIPSTSSIDCNTIMDKDIYIVRGQCKKVNTFIIYSATTVKAICTGVLNS-N 81
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EMBL; AF288642, AAG30414.2; -.
HSSP; P11916, 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana,
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
Purificiation and clouding of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog) ";
Nucleic Acids Res. 28:4097-4104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 VLSTTRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 15, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNasell ribonuclease precursor.
Rana castesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.4%; Score 280; DB 13; 48.6%; Pred. No. 1.3e-24; ative 14; Mismatches 35;
                                                                  132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 AA
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ProDom; PD000535; RnaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; AR351208; AAK30254.1; -
HSSP; P11916; 1BC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Conservative
                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8400;
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SIGNAL
                                                                                              Q98SM1;
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                               098SM1
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33 FWEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ODWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 QNWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"The identification of two novel ligands of the FGF receptor by a yeas: screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 132;
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                                                                                                                                                                                                                                                                                                                                                        Query Match
47.7%; Score 275.5; DB 13; Length
Best Local Similarity 44.1%; Pred. No. 4.3e-24;
Matches 49; Conservative 19; Mismatches 36; Indels
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA. InterPro; IPR01427; RNaseA. Pfam; PF00074; rnaseA; 1. Probom; PD000535; RNaseA; 1. SMART; SM00923; RNASE PC; 1. PROSITE; PS00127; RNASE_PANCREATIC; 1.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFROM 127; RNASA.
ProDon; P00074; rnaseA; 1.
ProDon; P000127; RNASE PA; 1.
PROSITE; PS00127; RNASE PA; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                             1 21 POTENTIAL.
22 132 RC-RNASEL1 RIBONUCLEASE.
132 AA; 14625 MW; D8D9A517452FBE53 CRC64;
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Last sequence update)
Last annotation update)
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EMBL; AF351207; AAK30253.1; -. EMBL; AF359578; AAL87036.1; -. HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                           22
132
                                                                                                                                                                                                                                                                                   132 AA;
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Best Local Similarity
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01-JUN-2001
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Q98SL8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 QNWATFQQKHITNTSSINCSNIMNNSLYIVGGQCKKVNTFIASSATTVKGICSG-VTDKK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";

J. MOL. Evol. 53:31-38(2001).

BENBL; AFS1210; AAK30256.1; -.

HSSP; P11916; 18C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
                                                                                                                                                                                                                                                    Rana cateŝbejana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
82 VLSTIRRQLANTCIRISITPRPCPYSSRIENNYICVKCENQYPVHFAGIGRC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Liver, Liao Y.-D., Jeng J.-T.; Liao Y.-D., Tang P.-C., Jeng J.-T.; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 POTENTIAL.
14615 MW; C8785B236B26E54E CRC64;
                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.5%; Score 286; DB 13; 47.7%; Pred. No. 2.6e-25;
                                                                                                                                133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                RNase A-type ribonuclease rc212 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.78;
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                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      NCBI TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                    Q98SL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q98SM2;
                                                                                                                            Q98SL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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298SM2
AC 298SS
AC 298SS
DT 01-JU
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QDWLTFQKKHLTNTRDVDCNNIMSTNLF----HCKDKNTF1YSRPEPVKAICKGIIASKN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 QTWAKFQQKHIPSTSSINCNTIMDNNIYIVGGQCKKVNTFIISSATTVKAICNG-VTNSN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ODWLTFOKKHLINIRDVDCNNIMSINLF----HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNase A-type ribonuclease rc218 precursor.

The stand catesbelana (Bull frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 VLTTSEFYLSDCN---VTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 VLSSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGOC 132
                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                            Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.8%; Score 282; DB 13; Length 1
46.8%; Pred. No. 7.7e-25;
ive 18; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
GO: GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA: 1.
SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                         132 RC-RNASE7.
14412 MW; 131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                      49.3%; Score 285; DB 13; 1 47.7%; Pred. No. 3.4e-25; tive 14; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 AA
                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1.
Prodom; PD000535; RnaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 P
14590 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
EMBL; AF351211; AAK30257.1; -
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Gaps

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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
                                                                      TISSUB=Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242556, AAG31442.2;
HSSP; P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 ODWDTFOKKHITDTKKVKCDVEMKKALFDCKKTNTFIFARPPRVQALCKNIKDNTNVLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 DVFYLPQCNRKKLPCHYRLDGSTNTICLTCMKELPIHFAGVGKC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                             GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                      14804 MW; AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 RC-RNASE6 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.6%; Score 298; DB 13; Best Local Similarity 49.5%; Pred. No. 1.1e-26; Matches 55; Conservative 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                ch 53.5%; Score 309; DB 13; 1 Similarity 53.8%; Pred. No. 5.4e-28; 56; Conservative 13; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 AA
                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
       Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                   128
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24 1
128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                         Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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       REPRESENTATION OF THE SQUEEN CONTRACT OF THE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 QDWETFQKKHLIDIKKVKCDVEMAKALFDCKKINTFIYALPGRVKALCKNIRDNIDVLSR 83
24 QNWETFQKKHLTDTRDVKCDAEMKKALFDCKQKNTFIYARPGRVQALCKNIIVSKAVLST 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                           01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
C1-CCT-2003 (TrEMBLrel. 25, Last annotation update)
C1-CTANaseal ribonuclease precursor.
Rana catesbeianal frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Anura, Neobatrachia, Ranoidea, Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-2003 (TENBELGE) 15, Last andcation update)
RC-RNase6 ribonuclease precursor.
Rama catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
Nucleic Arids Res. 28:4097-4104 (2000).
EMBL; AR242554; ARG31440.2; ---
HSSP; P22069; 10NC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Liver;
MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
                                                                      SEFYLSDCNVTSRPCKYKLKKSINTFCVTCENQAPVHFVGVGHC 104
                                                                                           35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 DAFLLPQCDRIKLPCHYKLSSSTWTICITCVNQLPIHFAGVGSC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC-RNASE3 RIBONUCLEASE.
2B14986082E0587D CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.8%; Score 311; DB 13; 54.8%; Pred. No. 3.2e-28;
                                                                                                                                                                                                                                128 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
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                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Liver;
MEDLINE=20512555; PubMed=11058105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57; Conservative
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                                                                                                                                                                                                                              PRELIMINARY;
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24 1
128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CUN-2001 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc208 precursor.
Rana catesbelana (Bull frog).
Ruha catesbelana (Bull frog).
Amphibja; Batrachia; Rordata; Craniata; Vertebrata; Euteleostomi;
Amphibja; Batrachia; Anura; Neobatrachia; Ranoidea; Rana NEI TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 VLTTSEFYLSDC---NVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                bullfrog, Rana catesbelana.";
J. Mol. Evol. 5:31-38(2001).
EMBL; AR351209; AR430255.1;
HSSP; P1916; Brod.
GO; GO:0004522; F:pucleic acid binding; IEA.
GO; GO:0004522; F:pucreatic ribonuclease activity; IEA.
InterPro; IPRO01427; RNASEA.
Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RNASE PE: 1.
PROSITE; PS00127; RNASE PE: 1.
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14628 MW; 87FCF122C3499E02 CRC64;
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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60
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                                                      Lidao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF242555; AAG31441.2; -.

EMBL; AF242555; AAG31441.2; -.

GO, GO:0003676; F:nucleic acid binding; IEA.

GO, GO:0004522; F:panoreatic ribonuclease activity; IEA.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
RC-RNase2 ribonuclease precursor.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 SEFYLAECNVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGIC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SEFYLSDCNVTSR-PCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.0%; Score 404.5; DB 13; Length 67.6%; Pred. No. 4.6e-39; Live 16; Mismatches 17; Indels
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989719CF52053ECC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                               Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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PROSITE; PS00127; RNASE PANCREATIC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 AA; 14724 MW;
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         SEQUENCE FROM N.A.
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SIGNAL
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24 QDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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Nucleic Acids Res. 28:4097-4104(2000).
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                                                                                               SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lido Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF392139; AAL54383.1;
PIR; A39035; A39035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 953F90D351CFEEF3 CRC64;
                                                                                                                                   SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGVGHC
                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                  127 AA
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ProDom, PD000535; RNaseA; 1.
SMART; SM0092; Naxae Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana pipiens (Northern leopard frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL 1 23 P
SEQUENCE 127 AA; 14469 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8404;
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SIGNAL
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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2004
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OM protein - protein search, using sw model

7, 2004, 21:29:10 ; Search time 29.5753 Seconds (without alignments) 1109.503 Million cell updates/sec Мау Run on:

US-09-961-400-2

578 1 QDWLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104 Perfect score: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

1017041 segs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL 25:* Database:

sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:* sp unclassified:* sp_rodent:*
sp_virus:*
sp_vertebrate:* _bacteriap:* _archeap:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:* sp_rvirus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Ogiava rana ninjen	OBUVX5 rana pipien	Ogdfv6 rana catesh	O9dfv8 rana catesb	Ogdfv7 rana catesh	Ogdfv5 rana catesh	O98sm0 rana catesb	098819 rana catesb	O98sm2 rana catesb	098sl8 rana catesb	098sml rana catesb	09df78 rana catesh	O9w738 xenonus lae	0861v3 pygathrix r	0861v2 pvgathrix h	0861v1 pydathrix a
		ID	0918V8	OBUVXS	Q9DFY6	Q9DFY8	O9DFY7	OSDEYS	Q98SM0	Q98SL9	Q98SM2	Q98SL8	Q98SM1	Q9DF78				
		DB	13	13	13	13	13	13	13	13	13	13	13	13	13	ø	9	9
		Length	127	127	129	128	128	128	133	133	132	133	132	132	169	146	146	146
dР	Query	Match	100.0	96.2	70.0	8.99	53.8	53.5	51.6	49.5	49.3	48.8	48.4	47.7	27.2	22.4	22.4	22.4
		Score	578	556	404.5	386	311	309	298	286	285	282	280	275.5	157.5	129.5	129.5	129.5
	Result	No.	; ; ; ;	2	m	4	5	9	7	89	6	10	11	12	13	14	15	16
		* Result Query	% Query Score Match Length DB ID	& Query Score Match Length DB ID 578 100.0 127 13 Q918V8	Auery Query Score Match Length DB ID Description 578 100.0 127 13 Q918V8 Q918V8 rana 556 96.2 127 13 O8UVX5 COBUXX5 rana	Score Match Length DB ID 578 100.0 127 13 Q91878 556 96.2 127 13 Q8UVX5 404.5 70.0 129 13 Q9EPF6	Score Match Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V6 386 66.8 128 13 Q9DFV8	Score Match Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V5 404.5 70.0 129 13 Q9DFV6 316 66.8 128 13 Q9DFV8 31 53.8 128 13 Q9DFV7	Score Match Length DB ID 578 100.0 127 13 2918V8 556 96.2 127 13 Q8UVX5 404.5 70.0 129 13 Q9DFY6 386 66.8 128 13 Q9DFY8 311 53.8 128 13 Q9DFY5 309 53.5 128 13 Q9DFY5	Score Match Length DB ID 578 100.0 127 13 Q91878 556 96.2 127 13 Q9UVX5 404.5 70.0 129 13 Q9DFY6 316 66.8 128 13 Q9DFY6 31 53.5 128 13 Q9DFY5 298 51.6 133 13 Q9BFY5	Acore Match Length DB ID 578 100.0 127 13 Q910V8 556 96.2 127 13 Q910V8 404.5 70.0 129 13 Q910V8 316 66.8 128 13 Q910V8 319 53.8 128 13 Q910V7 309 53.5 128 13 Q910V7 298 51.6 133 13 Q985V9 286 49.5 133 13 Q985V9	Acore Match Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V8 566 96.8 128 13 Q9DFY8 311 53.8 128 13 Q9DFY7 309 53.5 128 13 Q9DFY7 298 51.6 133 13 Q98SN0 286 49.5 133 13 Q98SN2 286 49.5 133 13 Q98SN2	Auch Length DB ID 578 100.0 127 13 291878 556 96.2 127 13 291878 556 96.2 127 13 291878 386 66.8 128 13 291878 311 53.8 128 13 291877 309 53.5 128 13 291877 309 53.5 128 13 291875 286 49.5 133 13 298580 287 49.3 132 13 298580 288 49.3 132 13 298580 288 49.3 132 13 298580	Acore Match Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V8 56.8 128 13 Q9DFY8 318 66.8 128 13 Q9DFY8 319 53.5 128 13 Q9DFY7 309 53.5 128 13 Q9DFY7 298 51.6 133 13 Q98SN0 286 49.5 133 13 Q98SN1 287 49.8 133 13 Q98SN1 280 48.8 133 13 Q98SN1 280 48.8 132 13 Q98SN1	Acore Match Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V8 386 66.8 128 13 Q9DFY8 311 53.8 128 13 Q9DFY8 309 53.5 128 13 Q9DFY8 309 53.5 128 13 Q9DFY8 288 49.5 133 13 Q98SN0 285 49.3 132 13 Q98SN1 285 49.3 132 13 Q98SN2 287 48.8 133 13 Q98SN3 275.5 47.7 132 13 Q98SN1	Score Match Length DB ID 578 100.0 127 13 2918V8 556 96.2 127 13 2918V8 586 66.8 128 13 2916V8 311 53.8 128 13 2916V8 309 53.5 128 13 2916V7 309 53.5 128 13 2916V7 286 49.5 133 13 2985N9 285 49.8 133 13 2985N8 282 48.8 133 13 2985N8 275.5 47.7 132 13 2995N8 157.5 27.2 169 13 2995N3	Acore March Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V8 556 96.2 127 13 Q918V8 311 53.8 128 13 Q9DFY6 309 53.5 128 13 Q9DFY7 309 53.5 128 13 Q9BFY7 286 49.5 133 13 Q98SM0 286 49.5 133 13 Q98SM2 287 48.8 133 13 Q98SM2 287 48.8 132 13 Q98SM2 287 48.8 132 13 Q98SM1 275 5 47.7 132 13 Q9BFY8 127.5 27.2 169 13 Q9M738 127.5 22.4 146 6 Q86M3	Acore Match Length DB ID 578 100.0 127 13 Q918V8 556 96.2 127 13 Q918V8 386 66.8 128 13 Q9DFY8 311 53.8 128 13 Q9DFY8 309 53.5 128 13 Q9DFY8 309 53.5 128 13 Q9DFY8 286 49.5 133 13 Q9BFY8 287 49.3 132 13 Q98SM2 287 49.3 132 13 Q98SM2 287 48.8 133 13 Q98SM2 275.5 47.7 132 13 Q98SM3 129.5 22.4 146 6 Q861Y2 129.5 22.4 146 6 Q861Y2

Q9jki5 mus saxicol Q9jki9 meriones un Q9jki7 mus saxicol	09/KJ3 meriones un 0861y4 trachypithe 09/Kj4 meriones un	291kjl meriones un 291kjl meriones un 27yrj6 balaena mys 291kj2 meriones un	Q9jkh9 mus pahari Q9jki3 mus saxicol	O91ki2 mus saxicol Q9tv25 eulemur ful O91ki2 mus saxicol		Oytsqe cercopithec Qytv32 gorilla gor Qytv45 galago moho O&hzeo pan troglod	Q97134 rattus norv Q9jkg6 mus caroli Q9jkg7 mus caroli	Q97130 mus musculu Q97125 mus musculu Q97kH8 mus pahari
1111	157 11 Q9JKJ3 146 6 Q861Y4 157 11 Q9JKJ4 167 11 OGTVTO	157 11 Q9JKJ1 147 6 Q7YRJ6 157 11 Q9JKJ2	11 9	11 9 11	111		155 11 Q9R134 156 11 Q9JKG6 156 11 Q9JKH7	1911
22.	126 21.8 125.5 21.7 125 21.6	122 21.1 121 20.9 121 20.9	120.5 20.8 119.5 20.7 118 20.4	116.5 20.2 115.5 20.0 115.5 20.0	10 10 10 1	113.5 19.6 113.5 19.6 113.5 19.6 113.5 19.6	HHH	112.5 19.5 112.5 19.5 112.5 19.5
11 14 14 14 14 14 14 14 14 14 14 14 14 1	2226	1 4 1 1 0 1 1 4 1 1 0	22 28 29	330	6 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	9 8 4 4 8 8 4 8 8 7 8 8	4 4 4 0 H 6	4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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MEDITRE=20330357; PubMed=10871370;

A Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;

The gender-specific mRNA encoding a cytocoxic ribonuclease contains a structure of gender-specific mRNA encoding a cytocoxic ribonuclease contains a structure of gender-specific mRNA encoding a cytocoxic ribonuclease contains a structure of gender structure.";

IN Nucleic Acids Res. 28:2375-2382(2000).

Rell, RH5513, AAP76935.1;

PIR, A39035, A39035.

R PSP; P22069; LONC.

R PSP; P22069; LONC.

R CO; GO:0003622; F:nucleic acid binding; IEA.

R CO; GO:0004622; F:nucleic ribonuclease activity; IEA.

R THCEPRO; IPR001427; RNaseA;

R Probon; P00074; rnaseA;

R PRODON; P000755; RNaseA;

R SMART; SM00092; RNAse_Pc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                      01-0cr-2000 (TrEMBLrel. 15, Created)
01-0cr-2000 (TrEMBLrel. 15, Last sequence update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
01-0cr-2003 (TrEMBLrel. 25, Last annotation update)
Onconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Rana pipiens (Northern leopard frog).
Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
NOBI_TaxID=8404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 POTENTIAL.
14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 578; DB 13;
100.0%; Pred. No. 3.5e-59;
tive 0; Mismatches 0;
                                      127 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 104; Conservative
                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
RESULT 1
                    0918V8
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1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 60

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TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser
OTHER INFORMATION: substitution (recombinant Met(-1) RaPLR1 Q1S)
US-09-948-391A-13
```

9; Gaps Query Match

47.1%; Score 285.5; DB 10; Length 105;
Best Local Similarity 50.0%; Pred. No. 1.2e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9;

1 MSNWATFQOKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NM 58

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Search completed: May 11, 2004, 14:39:23 Job time : 38.1719 secs

62 TTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110

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GENERAL INFORMATION:

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Sequence 13, Application US/09948391A Publication No. US20030027311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                    APPLICANT: Rybak, Susanna M. APPLICANT: Newton, Dianne L. APPLICANT: The United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rybak, Susanna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 97.2
Matches 106; Conservative
                                                                    US-09-948-391A-19
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                           TITLE OF INVENTION: IMMUNOCOMJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/109/961,400
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR PAPLICATION NUMBER: 09/622,613
PRIOR PLING DATE: 1090-08-17
PRIOR PLING DATE: 1090-03-26
PRIOR FILING DATE: 1990-03-26
PRIOR FILING DATE: 1990-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VOR: 2.1
SEQ ID NO S: 43
SOFTWARE: PATENTIN VOR: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NWAIFQQKHIINTFIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: INMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NWATFQQKHIINTPIICNTILDNNIYIVGGQCKRVNTFIISSATTVKALCTGVINLNVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 596; DB 10
Pred. No. 7e-60;
2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR PELING DATE: 1999-03-26
PRIOR PELING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09961400 Publication No. US20030124131A1
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.3%;
97.3%;
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Rana catesbeiana
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ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 98.3
Best Local Similarity 97.3
Matches 108; Conservative
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SEQ ID NO 19
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US-09-961-400-19
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Matches 107;
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3 NWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 110;
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                                                                                                                                 APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The Supremented by The Secretary of the
APPLICANT: Pepartment of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT APPLICATION NUMBER: US 60/079,751
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.5%; Score 585; DB 10;
97.2%; Pred. No. 1.2e-58;
tive 2; Mismatches 1;
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CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PARENTIN VET. 2.0
SEQ ID NO 13
LENGTH: 105
; Sequence 19, Application US/09948391A; Publication No. US20030027311A1; GENERAL INFORMATION:
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US-09-961-400-22
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: CELLS
FILE REPERENCE: 018733/1029
FILE REPERENCE: 018733/1029
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR PLILNG DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
9
                         1 MQNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVTTFIISSATTVKALCTGVINMNV 60
MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV
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                                                                                                                                      61 LSTTRFQLMTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCF 111
                                                                                                         LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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Sequence 21, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 012280-343110US
CURRENT FILING DATE: 1998-03-10

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1999-03-26

PRIOR FILING DATE: 1099-03-26

PRIOR FILING DATE: 1099-03-26

PRIOR FILING DATE: 1099-03-26

PRIOR FILING DATE: 1099-03-26

PRIOR FILING DATE: 1000-08-17

NUMBER OF SEQ ID NOS: 43

LENGTHAE: PATENTIN VORES: 2.0
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, Sequence 21, Application US/09961400
; Publication No. US20030124131A1
, GENERAL INFORMATION:
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Best Local Similarity
Matches 108; Conservat
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98.3%; Score 596; DB 10; Length 117;
Best Local Similarity 97.3%; Pred. No. 7e-60;
Matches 108; Conservative 2; Mismatches 1; Indels (
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APPLICANT: Rybak, Susanna M.
APPLICANT: Rybak, Susanna M.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the APPLICANT: as represented by The Secretary of the APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-34311005
FILE REFERENCE: 015280-34311005
CURRENT FILING DATE: 2002-05-10
PRIOR PRILING DATE: 2002-05-10
PRIOR FILING DATE: 1999-03-25
PRIOR FILING DATE: 1999-03-26
                                                                                                                                                                                                                                                                                                                                                                                 Score 596; DB 10;
Pred. No. 6.6e-60;
2; Mismatches 1;
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 21
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                         98.3%;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.33
Matches 108; Conservative
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Rana catesbeiana
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SEQ ID NO 15
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                                                                                                                                                                                                                                                                                                         Length 110;
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APPLICANT: Rybak, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-3431100S
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100.0%; Pred. No. 1.8e-60;
iive 0; Mismatches 0;
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CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR PILING DATE: 1999-03-27
PRIOR PILING DATE: 1999-03-26
PRIOR PLILING DATE: 1999-03-26
PRIOR PILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Rana catesbeiana
                                                                                                                                                                                                                                                                                                                                                  Matches 110; Conservative
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109; Conservative
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Best Local Similarity
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                                                                                                                                                                                      LENGTH: 110
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Best Local (
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98.5%; Score 597; DB 10; Length 1
Best Local Similarity 100.0%; Pred. No. 5e-60;
Matches 109; Conservative 0; Mismatches 0; Indels
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APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REPERENCE: 015500-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
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PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFFWARE: PATENTIN Ver. 2.0
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Publication No. US20030027311A1
GENERAL INFORMATION:
Sequence 15, Application US/09961400
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Best Local Similarity
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gequence 26, Application US/09961400

publication No. US20030124131A1

geneme 26, Application US/09961400

publication No. US20030124131A1

general information:

APPLICANT: RYBAK, SUSANNA M.

APPLICANT: OSLDENBERG, DAVID M.

APPLICANT: NEWTON, DIANNE L.

TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: UMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

TITLE OF INVENTION: CELLS

FILE REFERENCE: 018733/1059

CURRENT APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 09/622,613

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR APPLICATION NUMBER: 60/079,751

PRIOR PILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 43

SECTION NO. 26

NUMBER OF SEQ ID NOS: 43

SECTION NO. 26
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APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: US. 09/961,400
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR PEPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/79,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
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1 MSNWATFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
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                                                                                           ; DB 10; Length 111; 4.8e-61;
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Publication No. US20030124131A1
GENERAL INFORMATION:
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; ORGANISM: Rana catesbeiana
US-09-961-400-17
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Matches 111; Conservative
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                                                                                                       1 MSNWAJFQQKHIINTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNV 60
                                                                                                                                       1 MONWATFOOKHIINTPIICNTIMDNNIXIVGGOCKRVNTFIISSATTVKAICTGVINMNV 60
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APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: GOLDENBERG, DAVID M.
TITLE OF INVENTION: IMMUNCCONUTGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT FILLING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence: Rana OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution OTHER INFORMATION: (recombinant RaCOR1 Q1S)
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  Length 111;
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                                                  1; Indels
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Sequence 24, Application US/09948391A

Fublication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Dianne L.

APPLICANT: The United States of America

APPLICANT: The United States of America

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-3431100S

CURRENT APPLICATION NUMBER: US/09/948,391A

FRICH APPLICATION NUMBER: US 60/079,751

FRICH APPLICATION NUMBER: US 60/079,751

FRICH APPLICATION NUMBER: WO PCT/US99/06641

FRICH FILING DATE: 1999-03-26

FRICH APPLICATION NUMBER: WO PCT/US99/06641

FRICH FILING DATE: 1999-03-26

FRICH FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 43

SORUMARE: Patentin Ver. 2.0

SEQ ID NOS 44
Score 602; DB 10;
Pred. No. 1.4e-60;
0; Mismatches 1;
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; Publication No. US20030124131A1
; GENERAL INFORMATION:
99.3%;
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ORGANISM: Artificial Sequence
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Matches 110; Conservative
  Query Match
Best Local Similarity 99.1
Matches 110; Conservative
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US-09-948-391A-24
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US-09-961-400-24
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum DB seq length: 200000000
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Sequence 24, Sequence 15, Sequence 15, Sequence 26, Sequence Sequence Sequence Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-948-391A-26 US-09-961-400-26 US-09-961-400-17 US-09-961-400-17 US-09-961-400-24 US-09-961-400-15 US-09-961-400-15 US-09-948-391A-17 US-09-948-391A-17 US-09-961-400-21 US-09-961-400-22 US-09-961-400-22 US-09-961-400-22 US-09-961-400-22 US-09-961-400-22 US-09-961-400-19 US-09-961-400-19 US-09-961-400-19 US-09-961-400-19 US-09-961-400-19 US-09-961-400-19 SUMMARIES Query Match Length DB Result Š.

13,	Sequence 11, Appl Sequence 11, Appl Sequence 9, Appli Commence 2, Appli		Sequence 28, Appl Sequence 2, Appli Sequence 8, Appli	1	4.4	ω σ	u n	· m c	-	Sequence 89, Appl Sequence 139, App	141	Sequence 52, Appl	5,7	7
US-09-961-400-13 US-09-948-391A-6 US-09-961-400-6	US-09-948-5918-11 US-09-961-400-11 US-09-961-400-9 US-10-153-882-2	US-09-948-391A-28	US-09-961-400-28 US-09-948-391A-2 US-09-961-400-8	US-09-986-119-1 US-09-918-887-1	US-09-948-391A-4 US-09-961-400-4	US-09-948-391A-8 US-09-948-391A-9	US-10-461-713-53 US-09-986-119-3	US-09-918-887-3	7	US-10-016-248-89 US-10-074-978A-139	US-10-074-978A-141	US-10-461-713-52 TIS-09-731-879-254	9-87	US-09-981-286A-8
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285.5 281.5 281.5	280.5 278.5	276.5	276.5 275.5 275.5	272.5	270.5	266.5	264.5	206	135.5	126.5	121	117.5	117	114.5
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ALIGNMENTS

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Sequence 26, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susama M.
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: The United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 012280-343110US
CURRENT PELLORION NUMBER: US/09/948,391A
CURRENT FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1999-03-27
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: US/09/622,613
PRIOR APPLICATION NUMBER: US/09/622,613
FRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR APPLICATION NUMBER: WO SAME OF SAME
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54 ---GVINLNVLSTTRFQLNTCTRTSITPRP-CPYSSRTETNYICVKCEN--QYPVHFAGI 107
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20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                          Tragulus javanicus (Lesser Malay chevrotain).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Tragulina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                            21.2%; Score 128; DB 6; Length 170; 32.3%; Pred. No. 9.8e-07; Live 18; Mismatches 46; Indels
                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-type ribonuclease ribonuclease precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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Last annotation update)
                                 170 AA
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PROSITE; PS00127; RNASE_PANCREATIC; 1
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SEQUENCE FROM N.A.
STRAIN=NMRI;
MEDLINE=22493143; PubMed=12548285;
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PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
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                           PRELIMINARY;
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Best Local Similarity
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AC Q8028
DT 01-JU
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DE ANG10
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CO Eukar
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Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I., "Angiogenins: a new class of microbicidal proteins involved in innate immunity.";
                                                                                                                                                                                                                                                                                                                                                                                       34 CKRVNTFIISSATTVKAIC---TGVINLANV-LSTTRFQLNTCTRTSITP-RPCPYSSRTE
                                                                                                                                                                                                                                                                                                       21.1%; Score 127.5; DB 11; Length 144; 38.2%; Pred. No. 9.4e-07; tive 13; Mismatches 29; Indels 5;
                                                       | Nat. Immunol. 4:269-273 (2003). |
| Nat. Immunol. 4:269-273 (2003). |
| RMBL, AVIS10870; AA062254.1; -. |
| GO; GO:0004525; F:nucleic acid binding; IEA. |
| GO; GO:0004525; F:nucleic acid binding; IEA. |
| GO; GO:000427; RNaseA. |
| Fam; PF00744; RIBONUCLEASE. |
| ProDom; PD000535; RNaseA; 1. |
| SMART; SM00925; RNASeB. |
| PROSITE; PS00127; RNASE PANCREATIC; 1. |
| SPOSITE; PS00127; RNASE PANCREATIC; 1. |
| SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64; |
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122 FRYIVIACEDGWPVHF 137
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Best Local Similarity
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Xenopus laevis (African clawed frog)
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MEDLINE=96069863; PubMed=7585965;
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Best Local Similarity 39.3%,
Best Local 44; Conservative
                                                                                                                                                                       43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 FRL2 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 QDWETFQKKHLIDIKKVKCDVEMAKALF---DCKKINIFIYALPGRVKALCKNIRDNID 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242556; AAG31442.2; -.
HSSP; P22669; LOWC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                  C TISSUELLIVET.

C TISSUELLIVET.

MEDLINE=2051255; PubMed=11058105;

MEDLINE=2051255; PubMed=11058105;

Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;

"Purification and cloning of cytotoxic ribonucleases from Rana closesbeiana (bullface)";

"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullface)";

II. actesbeiana (bullface)";

Nucleic Acids Res. 28:4097-4104 (2000).

EMBL; AP242554; AAG31440.2;

Resp. P22069; 10NC.

Ros, Go.0003676; F.nucleic acid binding; IEA.

GO; GO:0003676; F.nucleic acid binding; IEA.

GO; GO:0004522; F.pancreatic ribonuclease activity; IEA.

Probom; PR00174; RNSSEA; I.

PROSITE: PS00127; RNSSEA; I.
                                                                                        RC-RNase3 ribonuclease precursor.
Rana catesbeiana (Buli frog).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 VLSRDAFLLPQCDRIKL.--PCHYKLSSSINTICITCVNQLPIHFAGVGSCP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                        36.9%; Score 223.5; DB 13; Length 128; 40.2%; Pred. No. 7.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             2B14986082E0587D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ©9DFYS;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                  RC-RNASE3 RIBONUCLEASE
                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AA
                          128 AA
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2001 (TrEMBLrel. 18, Last s 1-0CT-2003 (TrEMBLrel. 25, Last a RC-RNase6 ribonuclease precursor. Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                               14517 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                          PRELIMINARY;
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128
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24 1
128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                             NCBI TaxID=8400;
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                                        Q9DFY7;
                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                         Signal
                          09DFY7
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RESULT 11
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59
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                                                                                                                                                                                                                                                                                                                                                                                                                                               2 QNWATFQOKHILNT-PILCNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 VLSRDVFYLPQCNRKKL---PCHYRLDGSTNTICLTCMKELPIHFAGVGKCP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Cranīata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 LN-VLSTTRFQLNTCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 STFVISKELLPLTDCLLMGRTARPPNCAYNQTRTTGVINITCENNYPVHFAG 138
                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                              DB 13; Length 128;
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                                                                                                                                                                                                                                                                                                                        35.5%; Score 214.5; DB 13; Length 38.4%; Pred. No. 8.2e-17; ative 20; Mismatches 40; Indels
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GO, GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA.
Probom; PF000535; RNaseA.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003676; Fincleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR0427; RNaseA.
ProDon; P00074; rnaseA; 1.
ProDon; P000127; RNASE PANTRATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                          SIGNAL 1 23 POTENTIAL.
CHAIN 24 128 RC-RNASEG RIBONUCLEASE.
SEQUENCE 128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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us-09-961-400-21.rspt

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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; P0000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                48; Conservative
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                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                             23
129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                catesbeiana (bullfrog)
                                                                                                                      Local Similarity
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Matches 44; Conserv
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                     24 QDWLTFQKKHITNTRDVDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                        ONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                         45.2%; Score 273.5; DB 13; Length 127; 48.6%; Pred. No. 1.3e-23; tive 16; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wel C.W., Tang P.C., Wang S.C.
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBI, AF242555; AAG31441.2; -.
PDB; IKVZ; 28-JUL-02.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                            EMEL, AF3313139, AAL54383.1;
PIR, A39035, A39035.
PIR, A39035, A39035.
PIR, A39035, A39035.
PIR, Bancreatic acid binding, IEA.
GO, GO:0003676; F:nucleic acid binding, IEA.
InterPro, IPR001427; RNaseA.
Propon, PD000031; RNaseA.
PRODOM: PD00092; RNaseA.
PROSTIE; PS00127; RNASE PC, 1.
                                                                                                                                                                              Lião Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      POTENTIAL. 953F90D351CFEEF3 CRC64;
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Last annotation update)
                                                             Last sequence update)
Last annotation update)
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                                                 Created)
                                                                                                          Rana pipiens (Northern leopard frog)
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                          PRT;
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                                                                                                                                                                                                                                                                                                                                       SIĞNAL 1 23 P
SEQUENCE 127 AA; 14469 MW;
                                               01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                               54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                    Onconase precursor
                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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   RESULT 8
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                                                                                                                                                                                                           2 QNWATFQQKHIINT-PIICNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                                                                                               24 QDWATFKKKHILDTWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSAD 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P.-C., Wang S.-C.;
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                                                                                                                                                                                                                                                                                                                                                  80 VLSNSEFYLAEC---NVKPRKPCKYKLKKSSNRICIRCEHELPVHFAGVGICP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILINE-20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                     10;
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                                                                                                  Length 129;
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C Submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF24253; AAG31439.1; --
PDB; 1M58, 09-JAN-03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004227; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 128 RC-RNASE2 RIBONUCLEASE.
128 AA; 14839 MW; 989719CF52053ECC CRC64;
                                               826A62882B10ABDA CRC64;
                      RC-RNASE4 RIBONUCLEASE
                                                                                                                                                        30;
                                                                                                     DB 13;
                                                                                               40.2%; Score 243; DB 13;
42.5%; Pred. No. 4.3e-20;
tive 25; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%; Score 225.5; DB 1
39.3%; Pred. No. 4.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic Acids Res. 28:4097-4104 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                               14724 MW;
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3

Gaps

2;

Q98SM1;

Q98SM1

RESULT 5

CMS860

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2 QNWATPQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NLN 59
                                                                                                                                                                                                                                                                                                                                                     22 QNWAKEKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 QDWLTFQKKGLINTRDVDCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.,
"A gander-specific mRNA encoding a cytocoxic ribonuclease contains a
Nucleic Acids Res. 28:2375-2382(2000).

BMB. ARISE133; AAF76935.1; -.

PIR, A39035; A39035.

HSSP, P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ONWATFOOKHIINT-PIICNTILDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
0nconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                          60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                    60 VLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENGYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 127;
                                                                                                                                                                                                                                                        Length 132;
                                                                                                                                                                                                                                                                                             Indels
              GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
Prodo: PD000535; RNaseA.
PROSITE; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                            132 RC-RNASEL1 RIBONUCLEASE.
14625 MW; D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                  61.5%; Score 372; DB 13; I
64.9%; Pred. No. 6.5e-35;
tive 10; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.9%; Score 277.5; DB 13;
48.6%; Pred. No. 4.6e-24;
tive 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 AA
                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe_PC; 1.
PROSTIE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20330357; PubMed=10871370;
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                              132
P11916; 1BC4.
                                                                                                                                                                                                              132 AA;
                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54;
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                   Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q918V8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q918V8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF288642; AAG30414.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                          MEDLINE=21539506; PubMed=11683320;
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001);
EMBL. APS1208; ARK30254.1; -.
                                                                                                                                                                                                      Bukaryota, Metazoa, Chordaťa, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordaťa; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana,
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.,
"Purification and clonning of cytotoxic ribonucleases from Rana
catesbelana (bullifrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 444.5; DB 13; Length
Pred. No. 3e-43;
8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95D61760F729868E CRC64;
                                                                                                 01-UNY-2001 (TrEMBLrel. 17, Created)
01-UNY-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-007-2001 (TrEMBLrel. 16, Created)
01-007-2001 (TrEMBLrel. 18, Last sequence update)
01-007-2003 (TrEMBLrel. 12, Last annotation update)
RC-RNasell ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                      132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 28:4097-4104(2000).
                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 22 Pr
132 AA; 14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85; Conservative
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rissum=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
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SEQUENCE

Signal SIGNAL

Query Match

Local

Matches

7

à g 83

ð du 09DF78:

29DF78

RESULT 6

4,

Gaps

7;

Gaps

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09

Q98SM2

RESULT 2

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23 QNWATFQQKHITNTSSINCSNIMMNSLYIVGGQCKKVNTFIASSATTVKGICSGYTDKKV 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QNWATFQQKHIINTPII-CNTILDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINLNV
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbelana.";

J. Mol. Evol. 53:31-38 [2001].

EMBL; AF351210; AAK30256.1; -.

HSSP; P19916; 1B64.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

HICTPRO; IPR001427; RNaseA.

Prodom: PD000535; RNaseA.

Prodom: PD000535; RNase Pc; 1.

SMART; SM00092; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
BMBL; AFS51211; AAK30257.1; --.
HSSP; P11916; 1BC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 LSTTRFQLNTCTRISITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LSSTKFOLDICTRIFITPRPCPYSSRTETNYICVKCENOYPVHFAGIGOCP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LSTTRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.4%; Score 474.5; DB 13; Length 77.5%; Pred. No. 1.1e-46; Live 12; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IRRO1427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD00535; RNaseA; 1.
SMART; SM00922; RNASE Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      C8785B236B26E54E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 22 POTENTIAL.
133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.3%; Score 467.5; DB 13; 75.7%; Pred. No. 6.7e-46; Live 14; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 AA
                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                           22 P
14615 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 77.5
mes 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                           1
133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0UN-2001 (TrEMBLrel. 17, Created)
01-0UN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Neobatrachia; Ranoidea, Rana.
                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-Pype ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                    LSTTRFQLNTCTRISITPRPCPYSSRTENNYICVKCENQYPVHFAGIGRCP 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENOYPVHFAGIGRC 110
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Pred. No. 9.7e-48;
6; Mismatches 12; Indels 1;
                                   LSTTRFQLNTCTRTSITPRPCPYSSRIETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Liver;
Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
HSSP; P11916; 1BC4.
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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RC-RNASE7.
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
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SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
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23 132 RC
132 AA; 14412 MW;
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J. Mol. Evol. 53:31-38(2001).
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82.7%;
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Best Local Similarity
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Matches

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7, 2004, 21:29:10 ; Search time 31.566 Seconds (without alignments) 1109.503 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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SUMMARIES																	
SUMM	Q I	098SW0	Q98SM2	Q98SL9	G98SL8	Q98SM1	Q9DF78	Q918V8	QBUVX5	Q9DFY6	Q9DFY8	Q9DFY7	Q9DFY5	Q9W738	Q9BEC1	Q80Z85	Q80XS4
		13	13	13	13	13	13	13	13	13	13	13	13	13	9	11	11
	Query Match Length DB	133	132	133	133	132	132	127	127	129	128	128	128	169	170	144	1.53
d/o	Query Match	91.7	79.9	78.4	77.3	73.5	61.5	45.9	45.2	40.2	37.3	36.9	35.5	26.6	21.2	21.1	21.1
	Score	554.5	483.5	474.5	467.5	444.5	372	277.5	273.5	243	225.5	223.5	214.5	161	128	127.5	127.5
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Query Match
91.7%; Score 554.5; DB 13; Length 133;
Best Local Similarity 92.8%; Pred. No. 6.6e-56;
Matches 103; Conservative 2; Mismatches 5; Indels 1;

QYYZj6 balaena mys 2861y5 colobus gue Ogtvco sus scrofa Ogbdc2 antilocapra Ogwd94 berylmys bo Ogwd94 berylmys bo Ogwd94 berylmys bo Ogwd94 antilocapra Oyyzj5 tursiops tr Ogk2t2 mus musculu Og81y4 trachypithe Ogwd92 rattus exul Og861y4 bygathrix r Og861y2 bygathrix r Og861y2 bygathrix a Ogwd95 rattus norv Ogwc63 mus musculu Ogwd95 berylmys bo Ogwd95 argulus ja Ogwd95 ateles geof Ogwg06 ateles geof	te) date) rata; Buteleostomi; idea; Ranidae; Rana. ; ribonuclease from the vity; IEA.
6 QYYRJ6 6 Q86LY5 6 Q9TVC0 6 Q9TVC0 11 Q8VD94 11 Q8VD94 11 Q8VD94 6 Q7KJ2 11 Q8CGG3 11 Q8CGG3 11 Q8VD92 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q86LY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8CHY3 6 Q8TY3 6 Q8	ALIGNMENTS 1. 1 O98ENO PRELIMINARY; PRT; 133 AA. O98ENO; TEMBLE-1 17, Created) 01-JUN-2001 (TEMBLE-1 17, Last sequence update) 01-JUN-2001 (TEMBLE-1 17, Last sequence update) 01-OTT-2003 (TEMBLE-1 17, Last sequence update) 01-OTT-2003 (TEMBLE-1 17, Last sequence update) Nase A-type ribonuclease rc208 precursor. Rana catebelaiaa (Bull frog). Eukaryota; Meazoa; Chordata; Craniata; Vertebrata; Euteleo Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae (NEI Tax.D=8400; [1]. SEQUENCE PROM N.A. RADDILNE=21539566; PubMed=11683320; Rosenberg H.F., Zhang J., Liao YD., Dyer K.D.; RADDILNE=21539566; PubMed=11683320; Rosenberg H.F., Zhang J., Liao YD., pper K.D.; READIL FROG) AAX.0255.1; - "Rapid diversification of RNase A superfamily ribonuclease J. Mol. Evol. 53:31-38(2001). EMBL; AF351209; AAX.0255.1; - HSSP; Pl1916; 1BC4. GO; GO:0003676; Francreatic ribonuclease activity; IEA. HSSP; Pl1916; 1BC4. GO; GO:0004522; RNaseA; 1. SMART; SNO0092; RNASE PC; 1. PRODON; PRO0014; TRASE_PANCREATIC; 1. SMART; SNO0092; RNASE PC; 1. SIGNAL SIGNAL SIGNAL SIGNAL SIGNAL SIGNAL SIGNAL STANESSAN STANESE PC; 1. SIGNAL SIGNAL SIGNAL SIGNAL STANESSAN STANESE PC; 1.
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17 123.5 19 122.1 19 121.5 20 121.5 22 111.5 22 1118.5 24 1118.5 26 116.5 27 116.5 28 116.5 33 116.5 33 116.5 33 116.5 33 116.5 33 117.5 33 117.5 34 100.5 35 100.5 36 100.5 37 100.5 38 100.5 38 100.5 48 100.5 48 100.5 48 100.5 49 100.5 40 100.5 4	DIT 1 MOSSEMO PREL QOSSMO; O1-JUN-2001 (TrE O1-JUN-2001 (TrE O1-JUN-2001 (TrE C1-JUN-2001 (TrE C1-TOON (TRE CNASE A-type rib RANA CAtype rib RANA CATSON NCBI TAXID=8400; (NCBI TAXID=9000; (N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 CKNGQPNCHQSNST-MNITDCRQTGGSKYPNCAYKTSQKQKYIIVACEGTPSVPVHFDGS 141
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 POTENTIAL.
170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
18832 MW; AB6CETE1E5549AAO CRC64;
                                                                                           Tragulus javanicus (Lesser Malay chevrotain).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Tragulina,
Tragulidae, Tragulus.
                                                                                                                                                                                                                                                                                   (Tragulus javanicus).";
Eur. J. Biochem. 268:3890-3897(2001).
-!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
EMBL; AJ771299; CAC24723.1; -.
HSSP; P00656; 1LSQ.
                                                                                                                                                                                                                       MEDINE=21347458; PubMed=11453981; Brenkelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A., Warmels H.W., Beintema J.J., in the primitive ruminant chevrotain "Secretory ribonocleases in the primitive ruminant chevrotain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 170;
                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-type ribonuclease ribonuclease precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                             GO; GO:0004519; F:endonuclease activity; IEA.
GO; GO:0016787; F:hydroclase activity; IEA.
GO; GO:0004522; F:panoreatic ribonuclease activity; IEA.
Interpro; IPR001427; RNaseA.
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Last sequence update)
Last annotation update)
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           170 AA
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ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PS, 1.
Endonuclease; Hydrolase; Nuclease; Signal.
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SQUENCE FROM N.A.
STRAIN=NWRI;
MEDLINE=22493143; PubMed=12548285;
            PRT;
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            PRELIMINARY;
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20
170 AA;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
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62 CKDVNTFIHGTKKNIRALCGKKGSPYGENFRISNSPFQITTCTHSRGSPWPPCGYRAFKD 121
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Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I., "Angiogenins: a new class of microbicidal proteins involved in innate
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                        Query Match 21.2%; Score 128.5; DB 11; Length 144; Best Local Similarity 38.2%; Pred. No. 4.6e-07; Matches 29; Conservative 13; Mismatches 29; Indels 5;
                                                             Mat. Immunol. 4:269-273 (2003).

BMEL, AY219870; AAO62354.1; -
GO, GO:0004525; F:nucleic acid binding; IEA.
GO, GO:0004527; F:panoreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
PETAM; PR00794; RIBONUCLEASE.
PRINTS; PR00794; RIBONUCLEASE.
PRODOM; PD000535; RNaseA: 1.
SNART; SNA0092; RNASE PA: 1.
SNART; SNA0092; RNASE PANCREATIC; 1.
SEQUENCE 144 AA; 16554 MW; 09808807C00224C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: May 11, 2004, 14:36:30 Job time : 36.6606 secs
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|22 FRYIVIACEDGWPVHF 137
                                                  immunity.";
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FRL2 protein.
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Q9W738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Liver;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF242556, AAG31442.2;
HSSP; P22069; IONC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                               RC-RNase3 ribonuclease precursor.
Rana catesbbiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                    MEDLINE=20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 LSRDAFLLPQCDRIKL---PCHYKLSSSTNTICITCVNQLPIHFAGVGSCP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 36.6%; Score 221.5; DB 13; Length
| Similarity 40.5%; Pred. No. 5.7e-18;
45; Conservative 18; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; NaseA.
Pfam; PF00074; rnaseA; 1.
Probom; PD000535; RNaseA, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA; 14517 MW; 2B14986082E0587D CRC64;
                                                                              (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RC-RNASE3 RIBONUCLEASE
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1-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                          128 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                     catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
EMBL; AF242554; AAG31440.2; --
HSSP; P22069; 10NC.
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                                          PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                       NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
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                                                                                                       01-OCT-2001
                                                                                                                           01-OCT-2003
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                                                                                   01-MAR-2001
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                                        Q9DFY7
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RESULT 11
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3 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 DWDTFQKKHLTDTKKVKCDVEMKKALF----DCKKTNTFIFARPPRVQALCKNIKDNTNV 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development.";
Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 LSRDVFYLPQCNRKKL---PCHYRLDGSTNTICLTCMKELPIHFAGVGKCP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 N-VLSTTRFQLNTCTRISITPRP--CPYSSRIETNYICVKCENQYPVHFAG 106
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                                                                                                                                                                                                                                                                                                                          35.1%; Score 212.5; DB 13; Length 128; 38.7%; Pred. No. 6.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP
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                                                                                                                                                                                                                                                                                                                                                                                      40; Indels
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GO, GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
Pfan: PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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Kinoshita N., Kirschner M.W.;
Submitted (JUW.) 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AFISSIG6; AAD41901.1;
HSSP; P00656; 1LSQ.
                                                                                                                                                                                                        1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW; AFEBFD67D266C7C2 CRC64;
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
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PROSITE; PS00127; RNASE PANCREATIC; 1.
SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
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Last annotation update)
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38.7%; Pred. No. 2e-10;
iive 10; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AA
                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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MEDLINE=96069863; PubMed=7585965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                      43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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InterPro, IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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128 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                             1
24
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                                                                                     SEQUENCE
                                                                                                                Query Match
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SIGNAL
                                               Signal.
SIGNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 DWLIFQKKHITUTRDVDCDNIMSTNLF---HCKDKNTFIYSRPEPVKALCKGIIASKNV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF242555; AAG31441.2; -.
PDB; IKVZ; 28-JUL-02.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RC-RNase4 ribonuclease precursor.
Rana catebbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidee; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20512555; PubMed=11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbelana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.0%; Score 272.5; DB 13; Length 127; Best Local Similarity 49.1%; Pred. No. 6.3e-24; Matches 54; Conservative 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                               Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF332139; AAL54383.1; -. PIR; A39035; A39035. Go; GO:0003676; F:nucleic acid binding; IEA. GO; GO:0004522; F:nancreatic ribonuclease activity; IEA. InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                        SIGNAL 1 23 POTENTIAL.
SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                               Last sequence update)
Last annotation update)
                          127 AA
                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASE PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                        Liao Y.-D., Wang S.-C.; "Rana pipiens onconase genomic DNA.";
                                                                                                                Rana pipiens (Northern leopard frog).
                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                          PRT;
                                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                          PRELIMINARY;
                                                                                         Onconase precursor.
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                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                               Signal.
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                          Q8UVX5
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  RESULT 8
              Q8UVX5
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Iniao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR242553; AAG31439.1; --
PDB; 1M58; 09-JAN-03
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                 25 DWATEKKKHLIDIWDVDCDNLMPTSLF----DCKDKNTFIYSLPGPVKALCRGVIFSADV
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                                                                                                                       ch 39.8%; Score 241; DB 13; Length 129;
1 Similarity 42.9%; Pred. No. 3.1e-20;
48; Conservative 24; Mismatches 30; Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 15, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                     61 LSTITRPQLNTCTRISITPR-PCPYSSRIETNYICVKCENQYPVHFAGIGRCP 111
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 LSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVEECP 128
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989719CF52053ECC CRC64;
                                                               129 AA; 14724 MW; 826A62882B10ABDA CRC64;
                             RC-RNASE4 RIBONUCLEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AA
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ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCKEATIC; 1.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14839 MW;
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HSSP; P11916; 1BC4.
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                                                                                                                                                                                                                                       SEQUENCE
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SIGNAL
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF288642; AAG30414.2; -.
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                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
Rapid diversification of RNase A superfamily ribonuclease from the bullitrog, Mana catesbeiana.";
J. Mol. Evol. 53:31.38 (2001).
EMBL; AF351208; AAK30254.1;
HSSP; P11916; 1BC4.
HSSP; Finucleic acid binding; IEA.
                                                                                                                                                                                      RNase A-type ribonuclease rc204 precursor.

Fara catesbeiana (Bull frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

NCBI_TaxID=8400;
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Ranidae; Rana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STTRPQLXXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.2%; Score 443.5; DB 13; Length 78.0%; Pred. No. 7.3e-44; ive 7; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
95D61760F729868E CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                   132 AA
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ProDom; PD000535; RNaseA; 1.
SMART; SM0092; RNASe Pc; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
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MEDLINE=20512555; PubMed=11058105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RC-RNaseL1 ribonuclease precursor.
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14704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.2
Best Local Similarity 78.0
Matches 85; Conservative
                                                                                   PRELIMINARY;
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Q9DF78
                                      RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 NWAKFKEKHITSISSIDCNIIMDKAIYIVGGKCKERNIFIISSEDNVKAICSGVSPDRKE 82
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Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
"A gender-specific mRNA encoding a cytotoxic ribonuclease contains a 31 UTR of unusual length and structure.";
Nucleic Acids Res. 28:2375-2382(2000).
BMBL, AFIGE333; AAR76935.1; -.
HSSP; P22069; 10NC.
GO; GO:0003676; Finucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana pipiens (Northern leopard frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSTISFKLNTCIRDSITPRECEYHPSPDNNKICVKCEKOLPVHFVGIGKC 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 45.6%; Score 276.5; DB 13; Length 127; l Similarity 49.1%; Pred. No. 2.2e-24; 54; Conservative 15; Mismatches 32; Indels 9;
                                                                                                                                                                                                                                                                                                           Length 132;
                                                                                                                                                                                                                                                                                                                                                             27; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                     POTENTIAL.
RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                        Score 371; DB 13;
Pred. No. 2.1e-35;
                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127
                                                                      Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNASe Pc; 1.
PROSITE; PS00127; RNAŠE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onconase variant rapLR1 precursor.
                                                                                                                                                                                                                                                       14625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interrus, france, 1.
Probom, PD000535; RNase, 1.
Probom, PD000535; RNase, 1.
                                                                                                                                                                                                                                                                                                           61.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15,
                                                                                                                                                                                                                                                                                                                                                          72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                               22 1
132 AA;
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8404;
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62

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Q98SM2;

Q98SM2

RESULT 2

Q98SM2

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SSTRFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGGCP 133
                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                      $; Score 473.5; DB 1:
8; Pred. No. 2.3e-47;
11; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                              SIGNAL 1 22 P
SEQUENCE 133 AA, 14615 MW;
                                                                                                                                                                                                                                                         78.1%;
78.2%;
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                                                                                                                                                                                                                                                                                        86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                   MEDLINE=21339506; PubMed=11683320; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.; "Rapid diversification of Rwase A superfamily ribonuclease from the bullfrog, Rana catesbeian "; J. Mol. Evol. 53:31-38(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Ranoidea, Ranidae, Rana.
NCBL_TaxID=8400;
                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Rana.Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
              79.6%; Score 482.5; DB 13; Length 132; 84.3%; Pred. No. 2.1e-48; tive 5; Mismatches 11; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
                                                                                                                                                                                                                                                                                                                                                                                                                          Lido Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK30253.1; -.
HSSP; P11916; 1BC4.
GO; GO:0003676; P:nucleic acid binding; IEA.
GO; GO:0004522; F:nucleic acid binding; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC-RNASE7.
131A745187978687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-07N-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                     132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNase A-type ribonuclease rc212 precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                    (TrEMBLrel. 17, Created)
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                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 132 R
132 AA; 14412 MW;
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Best Local Similarity 84.3
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 WATFOOKHIINTPII-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                       PRELIMINARY;
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132
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           NCBI TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
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SEQUENCE

SIGNAL

CHAIN

Signal

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298SL9; 61S860

RESULT 3

Q98SL9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVL 61
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the full freep, Rana catesbelana.";
Julifreep, Rana catesbelana.";
J. Mol. Evol. 53:31-38(2001).

BMBL; AF351210; AAK30256.1; -.

BMBL; AF351210; AAK30256.1; -.

RMSP; P11916; IBR4.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0004522; F:panoreatic ribonuclease activity; IEA.

InterPro; IPR001427; RNaseA.

RP Fam; FP00074; rnaseA; 1.

RP ProDom; PD000535; RNaseA; 1.

RP ROSITE; SM00092; RNASE PC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 NWATFOOKHIINTPII-CNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVINMNVL
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Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullifrog, Rana catesbeiana.";
J. Mol. Evol. 5:31-38(2001);
EMBL; AF351211; AAK30257.1;
HSSP; P11916; 1BG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RNAse A-type ribonuclease rc218 precursor.
Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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76.4%; Pred. No. 1.5e-46;
Live 13; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
InterPro; IPR001427; RNaseA.
Propon; PD00074; rNaseA; 1.
SMART; SM00092; RNASeA; 1.
PROSITE; PS00127; RNASE_PC; 1.
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133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C8785B236B26E54E CRC64;
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May 11, 2004, 14:30:53 ; Search time 35.6606 Seconds (without alignments) 982.106 Million cell updates/sec
                                                                                                                                             US-09-961-400-26
606
1 MSNWATFQQKHIINTPIICN.....ICVKCENQYPVHFAGIGRCP 111
                                                                                                                                                                                                                                                                                   1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                    1017041 seqs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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sp_bhage:*
sp_plant:*
sp_rodent:*
sp_vrous:*
sp_vrus:*
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sp_vribhate:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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sp_human:*
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Maximum DB seq length: 2000000000
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Perfect score:
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STIMMARTES

		Description	Q98sm0 rana catesb	rana	ana	Q98s18 rana catesb	O98sml rana catesb	Q9df78 rana catesb	Q918v8 rana pipien	Q8uvx5 rana pipien	Q9dfy6 rana catesb	ana	Q9dfy7 rana catesb	Q9dfy5 rana catesb	Q9w738 xenopus lae	Q9bec1 tragulus ja	Q80z85 mus musculu	Q80xs4 mus musculu
SOMMAKIES		ID	0888W0	Q98SM2	Q98SL9	O98SL8	Q98SM1	Q9DF78	808I6Q	QBUVXS	Q9DFY6	Q9DFY8	Q9DFY7	Q9DFY5	Q9W738	Q9BEC1	. Q80Z85	. Q80XS4
		igth DB	133 13	132 13	133 13	133 13	132 13	132 13	127 13	127 13	129 13	128 13	128 13	128 13	169 13	170 6	144 11	153 11
	* Ouerv	Match Length DB	91.7	79.6	78.1	77.0	73.2	61.2	45.6	45.0	39.8	37.0	36.6	35.1	26.1	21.6	21.2	21.2
		Score	555.5	482.5	473.5	466.5	443.5	371	276.5	272.5	241	224.5	221.5	212.5	158	131	128.5	128.5
	Result	No.	н	7	3	4	Ŋ	9	7	80	9	10	11	1.2	13	14	15	16

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Gaps

1;

Query Match 91.7%; Score 555.5; DB 13; Length 133; Best Local Similarity 94.5%; Pred. No. 6.3e-57; Matches 104; Conservative 0; Mismatches 5; Indels 1;

qq à

Q7yrj6 balaena mys Q8vd94 berylmys bo Q8bd20 antilocapra Q9tvC0 sus scrofa Q8vd88 rattus norv Q861y4 trachypithe Q9bh14 antilocapra Q861y2 pygathrix r Q861y2 pygathrix r Q861y2 pygathrix a Q7yrj5 tursiops tr Q861y2 pygathrix a Q861y2 colobus gue Q861y2 tursiops tr Q861y5 colobus gue Q861y2 colobus gue Q861y2 mus musculu Q8061y2 rattus exul Q8062 rattus norv Q95ne6 bubalus bub Q80764 mus musculu Q8063 perylmys bo Q90495 berylmys bo Q90495 tragulus ja Q80405 lagothrix l Q80605 lagothrix l Q80605 lagothrix l Q80605 angulus ja Q80605 tragulus ja Q80605 tragulus ja		ate) ata; Euteleostomi; dea; Ranidae; Rana. bonuclease from the ity; IEA.
6 QYRUG6 6 Q9TUC0 11 Q8VD84 6 Q9TUC0 11 Q8VD88 6 Q861Y4 6 Q861Y2 6 Q861Y2 6 Q861Y2 6 Q861Y2 11 Q8CG3 11 Q8CG3 11 Q8VD92 11 Q8VD92 11 Q8VD95 6 Q8DB9 11 Q8VD95 6 Q8DB9 6 Q9DB9 6 Q9DB9 6 Q9DB9 6 Q9DB9 6 Q9DB9 6 Q9DB9 6 Q9DB9 6 Q9DB9 6 Q9DB0 6 Q9DBC3 6 Q8SQ06 6 Q9DC6 6 Q9DBC3 6 Q9DC6 6 Q9DBC3 6 Q9DC6 6 Q9	ALIGNMENTS	AA. update on update . ertebra Ranoic nily r: activi
17 127.5 21.0 147 126 20.8 150 20 20.8 150 20 20.7 163 20 20.7 164 20.7 125.5 20.7 164 20.7 122.5 20.2 122.5 20.2 146 20.7 122.5 20.2 146 20.7 122.5 20.2 146 20.7 122.5 20.2 146 20.7 122.5 20.2 146 20.7 120.5 10.9 149 20.7 120.5 10.9 149 20.7 120.5 10.5 10.5 10.5 10.5 10.5 10.5 10.5 1		B SK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ATFQQKHI-----INTPIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICT----
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20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;</pre>
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Wararyota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                            Tragulus javanicus (Lesser Malay chevrotain).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Traguliaa; Tragulidae; Tragulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Tragulus javanicus).";
Eur. J. Biochem. 268:3897(2001).
Eur. J. Endicklitz: BELONGS TO THE PANCKEATIC RIBONUCLEASE FAMILY.
EMBL; AJ271299; CAC24723.1; --
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21347458; PubMed=11453981;
Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
Breukelman H.J., Jehntema J.J.;
"Secretory ribonucleases in the primitive ruminant chevrotain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.8%; Score 131; DB 6; Length 170; 33.1%; Pred. No. 2.8e-07; tive 17; Mismatches 46; Indels
                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brain-type ribonuclease ribonuclease precursor (Fragment).
RNASE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004519; F:endomuclease activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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170 AA.
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PRINTS; PR00794; RIBONUCLEASE.

ProDom; PD000535; RNaseA; 1.

SMOART; SM00027; RNASE PC; 1.

PROSITE; PS00127; RNASE PANCREATIC; 1.

Endonuclease; Hydrolase; Nuclease; Signal.
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STRAIN=NMRI;
MEDLINE=22493143; PubMed=12548285;
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Best Local Similarity
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62 CKDVNTFIHGTKKNIRALCGKKGSPYGENFRISNSPFQITTCTHSRGSPWPPCGYRAFKD 121
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Hooper L.V., Stappenbeck T.S., Hong C.V., Gordon J.I.,
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                                                                                                                                                Match 21.4%; Score 128.5; DB 11; Length 144; Local Similarity 38.2%; Pred. No. 4.6e-07; Les 29; Conservative 13; Mismatches 29; Indels 5;
                               completed: May 11, 2004, 14:36:29
le : 36.3394 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase3 ribonuclease precursor.
Rana catesbelana (Bull frog).
Rana catesbelana (Bull frog).
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranaa.
NCBI_TAXID=8400;
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase6 ribonuclease precursor.
Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Neobatrachia; Ranidae; Rana.
NCBI_TAXID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
MEDLINE-20512555; PubMed=11058105;
Liao X.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
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Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 128;
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GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
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                                                                 128 AA.
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ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 28:4097-4104(2000).
EMBL; AF242554; AAG31440.2; -.
HSSP; P22069; 10NC.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     2 NWAIFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGV-INMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NWATFOOKHII--NTPIICN-TIMDNNIYIVGGOCKRVNTFI-ISSATTVKAICTGVINM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 NINAFMEKHIVKEGAETNCNQTIKDRNIRF-KNNCKFRNTFIHDTNGKKVKEMCAGIVKS
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=96069863; PubMed=7585965;
Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a yeast screening method and their activity in Xenopus development."; Cell 83:621-630(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 N-VLSTTRFQLNTCTRTSITPRP -- CPYSSRTEINYICVKCENQYPVHFAG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                   DB 13; Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 169;
                                                                                                                                                                                                                                                                                                                                                     40; Indels
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                    1 23 POTENTIAL.
24 128 RC-RNASEG RIBONUCLEASE.
128 AA; 14804 MW, AFEBFD67D266C7C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300127; RNASE PANCREATIC; 1.
169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
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                                                                                                                                                                                                                                                                                              Query Match 35.4%; Score 212.5; DB 1:
Best Local Similarity 38.7%; Pred. No. 6.3e-17;
Matches 43; Conservative 19; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 26.3%; Score 158; DB 13
1 Similarity 38.7%; Pred. No. 2e-10;
43; Conservative 10; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA
                                                                           Pfam; PF00074; rnaseA; 1.
ProDcm; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF159166; AAD41901.1; -. HSSP; P00656; 1LSQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00074; rnaseA; 1.
ProDom; PD00053; RNaseA; 1.
PROSITE; PS00127; RNASE PANCI
SEQUENCE 169 AA; 18851 MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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InterPro; IPR001427; RNaseA.
Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                               1
24
129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                        SEQUENCE
                                                                                                               Query Match
                                                   Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                      Q9DFY8
                                                                            CHAIN
                                                                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                         Q9DFY8
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EMBL, AF242555, AAG31441.2; --
PDB, 1KVZ; 28-JUL-02.
GO, GO:0003576; F:nucleic acid binding; IEA.
GO, GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NWAIFQQKHIINI-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBL_TaxID=8400;
                                                                                                              Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20212555; PubMed-11058105;
Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
"Purification and cloning of cytotoxic ribonucleases from Rana
catesbelana (Dullfrog).";
Nucleic Acids Res. 28:4097-4104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                          Query Match

45.3%; Score 272.5; DB 13; Length 127;
Best Local Similarity 49.1%; Pred. No. 6.2e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9;
                                                                                                                                                                                      Liac Y.-D., Wang S.-C.;
"Rana pipiens onconase genomic DNA.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF32139; AAL54383.1;
PIR, A39035; A39035.
FIR CO. GO: Finuclea caid binding; IEA.
GO: GO: 00004522: F: Piancreatic ribonuclease activity; IEA.
InterPro: IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                        SIGNAL 1 23 POTENTIAL.
SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 16, Created)
(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 AA
                               127 AA.
                                                                                                                                                                                                                                                                                                                    SMART; SM00092; RNASe_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RC-RNase4 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                           Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                              Onconase precursor
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                        NCBI_TaxID=8404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                               Signal
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                                                                                                                                                                                                                                                                                                                      SMART:
                                QBUVX5
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Q9DFY6
       RESULT 8
                      28UVX5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 NWATFOOKHIINT-PIICNTIMDNNIYIVGGOCKRVNTFIISSATTVKAICTGVI-NMNV 59
                                                                                                                                                                                                                                                   25 DWAJFKKKHLIDIWDVDCDNLMPISLF---DCKDKNTFIYSLPGPVKALCRGVIFSADV 80
                                                                                                                                                                                                          2 NWATFQQKHIINT-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
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                                                                                                                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                           60 LSTIRFQLNICTRISITPR-PCPYSSRIEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                           Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 LSTDEFYLSDCNRIKL---PCHYKLKKSSNTICITCENKLPVHFVAVBECP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 LSTTRFQLNTCTRISITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                        DB 13; Length 129;
                                                                                                  / Match 40.1%; Score 241; DB 13; Length 12
Local Similarity 42.9%; Pred. No. 3e-20;
1es 48; Conservative 24; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF242553; AAG31439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDB; 1M58; 09-JAN-03.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
RC-RNASE2 RIBONUCLEASE.
989719CF52053ECC CRC64;
                    RC-RNASE4 RIBONUCLEASE.
826A62882B10ABDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNase2 ribonuclease precursor.
Rana catesbeiana (Bull frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.4%; Score 224.5; DB 1
39.6%; Pred. No. 2.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.6%; Pred. Alswatches
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 28:4097-4104(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20512555; PubMed=11058105;
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128 AA; 14839 MW;
                                                    14724 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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2,

Gaps

2;

RESULT 5

1MS860

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2 NWAIFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV 59
                                                                                                                                                                                                                                                                                                                                                                  23 NWAKFKEKHITSTSSIDCNTIMDKAIYIVGGKCKERNTFIISSEDNVKAICSGVSPDRKE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 NWAIFQOKHIINI-PIICNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVI-NMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20330357; PubMed=10871370; Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.; Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.; "A gender-specific mRNA encoding a cytotoxic ribonuclease contains 3' UTR of unusual length and structure."; Nucleic Acids Res. 28:2375-2382(2000).

EMBL; AF165133; AAF76935.1; -.
PIR; A39035; A39035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onconase variant rapLR1 precursor.
Rana pipiens (Northern leopard frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                          60 LSTTRFQLNTCTRTSITPRPCPYSSRTEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                              60 LSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
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                                                                                                                                                                                                                                                 61.7%; Score 371; DB 13; Length 1
65.5%; Pred. No. 2e-35;
ive 9; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.0%; Score 276.5; DB 13; Length
49.1%; Pred. No. 2.1e-24;
ive 15; Mismatches 32; Indels
                GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP, P22069; IONC.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IPRO1427; RNaseA.
                                                                                                                                                                                         RC-RNASEL1 RIBONUCLEASE.
D8D9A517452FBE53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 AA; 14491 MW; B8511DC5407AB69B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 AA
                                                                                                                                                                          POTENTIAL.
                                                                    Pfam; PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00074; rnaseA; 1.
ProDom; PD000535; RNaseA; 1.
SWART; SM00092; RNAse_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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                                                                                                                                                                                                             132 AA; 14625 MW;
                                                      InterPro; IPR001427; RNaseA.
                                                                                                                                                                                                                       Query Match
Best Local Similarity
72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                        21
HSSP; P11916; 1BC4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8404;
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                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                        SIGNAL
                                                                                                                                                    Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF288642; AAG30414.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NWATFQQKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                   Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38[2001].
EMBL; AF351208; AAK30254.1; -.
                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc204 precursor.
Rana catesbeiana (Bull frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR.-2001 (TrEMBLrel. 16, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RC-RNaseL1 ribonuclease precursor.
Rana catesbeian (Bull frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20512555; PubMed=11058105; Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C., "Purification and cloning of cytotoxic ribonucleases from Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13; Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 STTRFQLNTCTRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 SITRFQLXXXTRTFITSRPCPYSSTKETNKICVKCENEYPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95D61760F729868E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.8%; Score 443.5; DB 78.0%; Pred. No. 7e-44;
                                                                        132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
                                                                                                        (TrEMBLrel. 17, Created)
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                                                                      PRT;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14704 MW;
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ProDom; PD000535; RNaseA; 1.
SMART; SMO0092; RNAse Pc; 1.
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                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                           NCBI_TaxID=8400;
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                                                                                                          01-JUN-2001
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RESULT 6

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Length 127;

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Pfam; PF00074; rnaseA;
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 WATFOOKHIINTPII-CNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLS
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"Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana.";
J. Mol. Evol. 53:31-38(2001).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc212 precursor.
Rana catebbeiana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBL_TaxID=8400;
                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annocation update)
RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
Rana catesbelana (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia, Anura; Neobatrachia; Ranoidea; Rania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,
                                            80.3%; Score 482.5; DB 13; Length 132; 84.3%; Pred. No. 2e-48; ive 5; Mismatches 11; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTRFQLDTCTRTSITPRPCPYSSKKETNKICVKCENQLPVHFAGIGKC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ITRFQLNTCTRISITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
                     STTREQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liao Y.-D., Tang P.-C., Jeng J.-T.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF351207; AAK30253.1; -.
EMBL; AF359578; AAL87036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P11916; 1BC4.
GO; GO:0003676; F:nucleic acid binding: IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
InterPro; IFR01427; RNaseA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RC-RNASE7.
: 131A745187978687 CRC64;
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                                                                                                                                                                132 AA.
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
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MEDLINE=21539506; PubMed=11683320;
                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
MEDLINE=21539506; PubMed=11683320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
"Rapid diversification of RNase A superfamily ribonuclease from the builfrog, Rana catesbelana.";
J. Mol. Bvol. 53:31-38 (2001).
EMBL; AF351210; AAK30256.1;
HSSP; P19156; BRG.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
Interpre, IPR001427; RNaseA.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNase A-type ribonuclease rc218 precursor.
Rna catesbelaina (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniaes; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 STTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 STIRFQINICIRISITPRPCPYSSRIEINYICVKCENQYPVHFAGIGRCP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 SSTKFQLDICTRIFITPRPCPYSSRTETNYICVKCENQYFVHFAGIGQCF 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 78.8%; Score 473.5; DB 13; Length I Similarity 78.2%; Pred. No. 2.2e-47; 86; Conservative 11; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0004522; F:pancreatic ribonuclease activity; IEA
InterPro; IPR001427; RNaseA.
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133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C8785B236B26E54E CRC64;
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76.4%; Pred. No. 1.5e-46;
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SMART; SM00092; RNASe_PC; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
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PROSITE; PS00127; RNASE_PANCREATIC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
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133 AA; 14615 MW;
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ProDom; PD000535; RNaseA; 1.
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les 84; Conservative
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May 11, 2004, 14:30:53 ; Search time 35.3394 Seconds (without alignments) 982.106 Million cell updates/sec
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		Description	098sm0 rana catesb	rana	rana	rana	098sml rana catesh	09df78 rana catesb	0918v8 rana pipien	O8uvx5 rana pipien	Ogdfv6 rana catesb	O9dfv8 rana catesb	O9dfy7 rana catesb	09dfv5 rana catesb	O9w738 xenopus lae	O9bec1 tragulus ja	O80z85 musculu	Q80xs4 mus musculu
SCMMARIES		ID	098SM0	O98SM2	098SL9	098SL8	Q98SM1	Q9DF78	878I6Q	QBUVXS	Q9DFY6	Q9DFY8	Q9DFY7	Q9DFY5	Q9W738	Q9BEC1	Q80Z85	Q80XS4
		DB	13	13	13	13	13	13	13	13	13	13	13	13	13	9	11	11
		guery Match Length DB	133	132	133	133	132	132	. 127	127	129	128	128	128	169	170	144	153
	o*0	Match	92.4	80.3	78.8	77.6	73.8	61.7	46.0	45.3	40.1	37.4	36.9	35.4	26.3	21.8	21.4	21.4
		Score	555.5	482.5	473.5	466.5	443.5	371	276.5	272.5	241	224.5	221.5	212.5	158	131	128.5	128.5
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117 118 120 120 120	22 23 25 25 26	27 28 30 31		8 6 6 4 4 4 4 4 4 8 8 9 9 9 11 12 12 14 15

ALIGNMENTS

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Stomi; Rana.	3; 1; Gaps	
;; Euteleostomi;;; Ranidae; Rana muclease from tl	Length 133; Indels 1;	SSATTVKAIC
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reated) ast sequence ast sequence ast sequence ast annotati 08 precursor; Craniata; V eobatrachia, o YD., Dye se A superfa d binding; I ribonuclease EATIC; 1. POTENTIAL. B7FCF122C3.	Score 555.5; DB Pred. No. 6e-57; 0; Mismatches	NIYIVGG(NIYIVGG(
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PRELIMINARY; PRT; 133 AA. 1UN-2001 (TrEMBLrel. 17, Created) DCT-2003 (TrEMBLrel. 17, Last sequence up DCT-2003 (TrEMBLrel. 25, Last annotation se A-type ribonuclease rc208 precursor. a catesbeiana (Bull frog). 1Tyota; Metacon; Chordata; Craniata; Vert Inbia; Barrachia; Anura; Neobatrachia; Rat LINE=21539506; PubMed=11683320; JENCE FROM N.A. JENEE FROM N.A. JENEE FROM N.A. JENEE FROM N.A. JENEE 2539506; PubMed=11683320; JENEE FROM N.A. JAN 1000	imilarit ; Conse	NWATFOOK NWATFOOK
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